

MOLECULE TYPE:  
DESCRIPTION: peptide  
HYPOTHETICAL: NO  
US-08-946-525-4

Query Match 36.6%; Score 26; DB 3; Length 9;  
Best Local Similarity 80.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 HYPG 10  
DB 2 HIGPG 6

RESULT 27  
US-09-082-279B-920  
Sequence 920, Application US/09082279B  
Patent No. 6258782  
GENERAL INFORMATION:  
APPLICANT: Barney, Shawn  
APPLICANT: Guthrie, Kelly  
APPLICANT: Merutka, Gene  
APPLICANT: Arner, Mohamed  
APPLICANT: Lambert, Dennis  
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
FILE REFERENCE: 7872-043  
CURRENT APPLICATION NUMBER: US/09/082,279B  
CURRENT FILING DATE: 1998-05-20  
NUMBER OF SEQ ID NOS: 1515  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 920  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Core polypeptide  
US-09-082-279B-920

Query Match 36.6%; Score 26; DB 3; Length 9;  
Best Local Similarity 80.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 YGPGW 11  
DB 1 YGMGW 5

RESULT 28  
US-09-315-304B-920  
Sequence 920, Application US/09315304B  
Patent No. 6348568  
GENERAL INFORMATION:  
APPLICANT: Barney, S.  
APPLICANT: Guthrie, K.  
APPLICANT: Merutka, G.  
APPLICANT: Arner, M.  
APPLICANT: Lambert, D.  
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC  
FILE REFERENCE: 7872-052  
CURRENT APPLICATION NUMBER: US/09/315,304B  
CURRENT FILING DATE: 1999-05-20  
PRIOR APPLICATION NUMBER: 09/082,279  
PRIOR FILING DATE: 1998-05-20  
NUMBER OF SEQ ID NOS: 1667  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 920  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Core polypeptide

US-09-315-304B-920

Query Match 36.6%; Score 26; DB 4; Length 9;  
Best Local Similarity 80.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 YGPGW 11  
DB 1 YGMGW 5

RESULT 29  
US-09-599-286-4  
Sequence 4, Application US/09599286  
Patent No. 6447778  
GENERAL INFORMATION:  
APPLICANT: Arye Rudinstein, Barry R. Bloom, Yair Devash and Stanley J.  
City  
TITLE OF INVENTION: PEPTIDE COMPOSITIONS FOR THE TREATMENT AND  
PREVENTION OF HIV  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Amster, Rothstein & Epenstein  
STREET: 90 Park Avenue  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Word Processor (ASCII)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/599,286  
FILING DATE: 22-Jun-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/946,525  
FILING DATE: October 7, 1997  
APPLICATION NUMBER: 08/785,696  
FILING DATE: January 17, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Bogosian, Elizabeth A  
REGISTRATION NUMBER: 39,911  
REFERENCE/DOCKET NUMBER: 96700/448  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 697-5595  
TELEFAX: (212) 286-0854 or 286-0082  
TELEX: TWX 710-581-4766  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: <Unknown>  
DESCRIPTION: peptide  
HYPOTHETICAL: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-599-286-4

Query Match 36.6%; Score 26; DB 4; Length 9;  
Best Local Similarity 80.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 HYPG 10  
DB 2 HIGPG 6

RESULT 30  
US-09-834-784-920

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; Sequence 920, Application US/09834784
; Patent No. 6562787
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/834,784
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 920
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Core polypeptide
US-09-834-784-920

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Query Match          36.6%; Score 26; DB 4; Length 9;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

QY 7 YGPGW 11
DB 1 YGWGM 5

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RESULT 31
US-09-515-965A-920
; Sequence 920, Application US/09515965A
; Patent No. 6623741
; GENERAL INFORMATION:
; APPLICANT: Antczak, J.
; APPLICANT: Delmedico, M.
; APPLICANT: Erickson, J.
; APPLICANT: Lambert, D.
; APPLICANT: Sistra, P.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
; FILE REFERENCE: 7872-073
; CURRENT APPLICATION NUMBER: US/09/515,965A
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1994
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 920
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-515-965A-920

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```

Query Match          36.6%; Score 26; DB 4; Length 9;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

QY 7 YGPGW 11
DB 1 YGWGM 5

```

RESULT 32

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US-09-350-641C-920
; Sequence 920, Application US/09350641C
; Patent No. 6656906
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Atwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-067
; CURRENT APPLICATION NUMBER: US/09/350,641C
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 920
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-350-641C-920

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```

Query Match          36.6%; Score 26; DB 4; Length 9;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

QY 7 YGPGW 11
DB 1 YGWGM 5

```

```

RESULT 33
US-08-250-789A-94
; Sequence 94, Application US/08250789A
; Patent No. 5635597
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Chernov-Rogan, Tania
; APPLICANT: Davis, Ann M.
; TITLE OF INVENTION: Peptides That Bind to IL-2 Receptors
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend Hourie and Crew
; STREET: One Market Plaza, Stewart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/250,789A
; FILING DATE: 27-MAY-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5635597-1e1, Vernon A.
; REGISTRATION NUMBER: 32,483
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids

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TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-250-789A-94

Query Match 36.6%; Score 26; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 YGPG 10  
Db 2 YGPG 5

RESULT 34  
US-08-341-219-15  
Sequence 15, Application US/08341219  
Patent No. 5643877  
GENERAL INFORMATION:  
APPLICANT: Zohar, Y.  
APPLICANT: Rivier, J.  
APPLICANT: Powell, J.  
APPLICANT: Sherwood, N.  
APPLICANT: Gochliff, Y.  
TITLE OF INVENTION: Compounds and Methods For Controlling  
TITLE OF INVENTION: Reproduction in Fish  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: N.Y.  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/341,219  
FILING DATE: 05-DEC-1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30742  
REFERENCE/DOCKET NUMBER: 8399-003-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
OTHER INFORMATION: /product= "OTHER"  
OTHER INFORMATION: /label= Gly1  
OTHER INFORMATION: /note= "pyroglutamic acid"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 10  
OTHER INFORMATION: /product= "OTHER"  
OTHER INFORMATION: /label= Gly10  
OTHER INFORMATION: /note= "amidated"  
US-08-341-219-15

Query Match 36.6%; Score 26; DB 1; Length 10;  
Best Local Similarity 42.9%; Pred. No. 3.1e+02;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 KHYGPGW 11  
Db 1 EHWMSGW 7

RESULT 35  
US-08-341-219-16  
Sequence 16, Application US/08341219  
Patent No. 5643877  
GENERAL INFORMATION:  
APPLICANT: Zohar, Y.  
APPLICANT: Rivier, J.  
APPLICANT: Powell, J.  
APPLICANT: Sherwood, N.  
APPLICANT: Gochliff, Y.  
TITLE OF INVENTION: Compounds and Methods For Controlling  
TITLE OF INVENTION: Reproduction in Fish  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: N.Y.  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/341,219  
FILING DATE: 05-DEC-1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30742  
REFERENCE/DOCKET NUMBER: 8399-003-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
OTHER INFORMATION: /product= "OTHER"  
OTHER INFORMATION: /label= Gly1  
OTHER INFORMATION: /note= "pyroglutamic acid"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 10  
OTHER INFORMATION: /product= "OTHER"  
OTHER INFORMATION: /label= Gly10  
OTHER INFORMATION: /note= "amidated"  
US-08-341-219-16  
Query Match 36.6%; Score 26; DB 1; Length 10;  
Best Local Similarity 42.9%; Pred. No. 3.1e+02;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 KHYGPGW 11  
: : :  
Db 1 EHMWSHW 7

## RESULT 36

US-08-253-030-23  
; Sequence 23, Application US/08253030  
; Patent No. 5712373

GENERAL INFORMATION:  
APPLICANT: EDA, Yasuyuki  
APPLICANT: OSATOMI, Kiyoshi  
APPLICANT: SHIOSAKI, Kouichi  
APPLICANT: TOKIOSHI, Sachio  
APPLICANT: MATSUSHITA, Shuzo  
APPLICANT: HATTORI, Toshio  
APPLICANT: TAKATSUKI, Kiyoshi  
TITLE OF INVENTION: HIV Monoclonal Antibody  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/253,030  
FILING DATE: 02-JUN-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07\723,916  
FILING DATE: 01-JUL-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 175075/1990  
FILING DATE: 02-JUL-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 188300/1990  
FILING DATE: 16-JUL-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 74129/215/AOPA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-253-030-23

Query Match 36.6%; Score 26; DB 1; Length 10;  
Best Local Similarity 80.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 HYGPG 10  
: : :  
Db 1 HIGPG 5

RESULT 37  
US-08-253-030-25  
; Sequence 25, Application US/08253030  
; Patent No. 5712373

GENERAL INFORMATION:  
APPLICANT: EDA, Yasuyuki  
APPLICANT: OSATOMI, Kiyoshi  
APPLICANT: SHIOSAKI, Kouichi  
APPLICANT: TOKIOSHI, Sachio  
APPLICANT: MATSUSHITA, Shuzo  
APPLICANT: HATTORI, Toshio  
APPLICANT: TAKATSUKI, Kiyoshi  
TITLE OF INVENTION: HIV Monoclonal Antibody  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/253,030  
FILING DATE: 02-JUN-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07\723,916  
FILING DATE: 01-JUL-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 175075/1990  
FILING DATE: 02-JUL-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 188300/1990  
FILING DATE: 16-JUL-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 74129/215/AOPA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-253-030-25

Query Match 36.6%; Score 26; DB 1; Length 10;  
Best Local Similarity 80.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 HYGPG 10  
: : :  
Db 2 HIGPG 6

RESULT 38  
US-08-425-069-19  
; Sequence 19, Application US/08425069  
; Patent No. 5728810  
GENERAL INFORMATION:  
APPLICANT: Lewis, Randolph V.  
APPLICANT: Xu, Ming  
APPLICANT: Hittman, Michael B.  
TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK  
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL  
CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:



ADDRESSEE: Birch, Stewart, Kolasch & Birch  
STREET: 301 No. 5728th10th Washington Street  
CITY: Falls Church  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22046  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/425,069  
FILING DATE: 19-APR-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Murphy Jr., Gerald M  
REGISTRATION NUMBER: 28,977  
REFERENCE/DOCKET NUMBER: 1447-106P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 205-8000  
TELEFAX: (703) 205-8050  
TELEX:  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Araneus gemmoides  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..10  
OTHER INFORMATION: /label=fragment  
OTHER INFORMATION: /note="fragment of sequence from Araneus dragline  
OTHER INFORMATION: silk protein."  
US-08-425-069-19

Query Match 36.6%; Score 26; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 YGPG 10  
Db 3 YGPG 6  
RESULT 39  
US-08-687-559-10  
Sequence 10, Application US/08687559  
Patent No. 5955647  
GENERAL INFORMATION:  
APPLICANT: Fitcher, John H.  
APPLICANT: Beachy, Roger N.  
TITLE OF INVENTION: METHOD FOR USING TOBACCO MOSAIC VIRUS TO  
TITLE OF INVENTION: OVERPRODUCE PEPTIDES AND PROTEINS  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: US  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/687,559

FILING DATE: No. 5955647ember 18, 1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/01467  
FILING DATE: 03-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Leach, June M.  
REGISTRATION NUMBER: 31,238  
REFERENCE/DOCKET NUMBER: 07302/011001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-678-5070  
TELEFAX: 619-678-5099  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-687-559-10

Query Match 36.6%; Score 26; DB 2; Length 10;  
Best Local Similarity 80.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 HYPG 10  
Db 3 HIGPG 7  
RESULT 40  
US-08-317-844B-19  
Sequence 19, Application US/08317844B  
Patent No. 5989894  
GENERAL INFORMATION:  
APPLICANT: Lewis, Randolph V.  
APPLICANT: Xu, Ming  
APPLICANT: Himmann, Michael B.  
TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK  
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL  
CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF  
NUMBER OF SEQUENCES: 62  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Birch, Stewart, Kolasch & Birch  
STREET: 301 No. 5989894th Washington Street  
CITY: Falls Church  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22046  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/317,844B  
FILING DATE: 04-OCT-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Murphy Jr., Gerald M  
REGISTRATION NUMBER: 28,977  
REFERENCE/DOCKET NUMBER: 1447-105P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 241-1300  
TELEFAX: (703) 241-2848  
TELEX: 248345  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:

ORGANISM: Araneus gemmoides  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..10  
OTHER INFORMATION: /label= fragment  
OTHER INFORMATION: /note= "fragment of sequence from Araneus dragline"  
OTHER INFORMATION: silk protein."

US-08-317-844B-19  
Query Match 36.6%; Score 26; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 YGPG 10  
DB 3 YGPG 6

RESULT 41  
US-08-946-525-15  
Sequence 15, Application US/08946525  
Patent No. 6139843  
GENERAL INFORMATION:  
APPLICANT: Ayle Rubinstein, Barry R. Bloom, Yair Devash and Stanley J. Cryz  
TITLE OF INVENTION: PEPTIDE COMPOSITIONS FOR THE TREATMENT AND  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amster, Rothstein & Ebersstein  
STREET: 90 Park Avenue  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Word Processor (ASCII)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/946,525  
FILING DATE: October 7, 1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/785,696  
FILING DATE: January 17, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Bogosian, Elizabeth A  
REGISTRATION NUMBER: 39,911  
REFERENCE/DOCKET NUMBER: 96700/448  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 697-5995  
TELEFAX: (212) 286-0854 or 286-0082  
TELEX: TWX 710-581-4766  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
DESCRIPTION: peptide  
HYPOTHETICAL: NO  
US-08-946-525-15

Query Match 36.6%; Score 26; DB 3; Length 10;  
Best Local Similarity 80.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 6 HYPG 10  
DB 2 HYPG 6

RESULT 42  
US-08-912-314A-15  
Sequence 15, Application US/08912314A  
Patent No. 6210927  
GENERAL INFORMATION:  
APPLICANT: Zohar, Y.  
APPLICANT: Rivier, J.  
APPLICANT: Powell, J.  
APPLICANT: Sherwood, N.  
APPLICANT: Gochliff, Y.

TITLE OF INVENTION: Compounds and Methods For Controlling  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: N.Y.  
COUNTRY: USA  
ZIP: 10036-2711

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentia Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/912,314A  
FILING DATE: 30-JUN-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/341,219  
FILING DATE: 05-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30742  
REFERENCE/DOCKET NUMBER: 8399-003-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO

FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
OTHER INFORMATION: /product= "OTHER"  
OTHER INFORMATION: /label= Gly10  
OTHER INFORMATION: /note= "pyroglutamic acid"  
NAME/KEY: Modified-site  
LOCATION: 10  
OTHER INFORMATION: /product= "OTHER"  
OTHER INFORMATION: /label= Gly10  
OTHER INFORMATION: /note= "amidated"

US-08-912-314A-15  
Query Match 36.6%; Score 26; DB 3; Length 10;  
Best Local Similarity 42.9%; Pred. No. 3.1e+02;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 5 KHYPGW 11  
DB 1 EHWSHGW 7

RESULT 43

US-08-912-314A-16  
; Sequence 16, Application US/08912314A  
; Patent No. 6210927  
; GENERAL INFORMATION:  
; APPLICANT: Zohar, Y.  
; APPLICANT: Rivier, J.  
; APPLICANT: Powell, J.  
; APPLICANT: Sherwood, N.  
; APPLICANT: Gochilf, Y.  
; TITLE OF INVENTION: Compounds and Methods For Controlling  
; TITLE OF INVENTION: Reproduction in Fish  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: N.Y.  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/912,314A  
; FILING DATE: 30-JUN-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/341,219  
; FILING DATE: 05-DEC-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cornuzzi, Laura A.  
; REGISTRATION NUMBER: 30742  
; REFERENCE/DOCKET NUMBER: 8399-003-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8664/9741  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 1  
; OTHER INFORMATION: /product= "OTHER"  
; OTHER INFORMATION: /label= Glu1  
; OTHER INFORMATION: /note= "pyroglutamic acid"  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 10  
; OTHER INFORMATION: /product= "OTHER"  
; OTHER INFORMATION: /label= Gly10  
; OTHER INFORMATION: /note= "amidated"  
US-08-912-314A-16  
Query Match 36.6%; Score 26; DB 3; Length 10;  
Best Local Similarity 42.9%; Pred. No. 3.1e+02;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 5 KAYGPGM 11  
; : : :  
Db 1 EHMSHGM 7  
RESULT 44  
US-09-599-286-15  
; Sequence 15, Application US/09599286

Patent No. 6447778  
; GENERAL INFORMATION:  
; APPLICANT: Aye Rubinstei, Barry R. Bloom, Yair Devash and Stanley J.  
; CITY:  
; TITLE OF INVENTION: PEPTIDE COMPOSITIONS FOR THE TREATMENT AND  
; PREVENTION OF HIV  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amster, Rothstein & Ebenstein  
; STREET: 90 Park Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Word Processor (ASCII)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/599,286  
; FILING DATE: 22-Jun-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/946,525  
; FILING DATE: October 7, 1997  
; APPLICATION NUMBER: 08/785,696  
; FILING DATE: January 17, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bogosian, Elizabeth A  
; REGISTRATION NUMBER: 39,911  
; REFERENCE/DOCKET NUMBER: 96700/448  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 697-5995  
; TELEFAX: (212) 286-0854 or 286-0082  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: <Unknown>  
; DESCRIPTION: peptide  
; HYPOTHETICAL: NO  
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
US-09-599-286-15  
Query Match 36.6%; Score 26; DB 4; Length 10;  
Best Local Similarity 80.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 6 HYRPG 10  
; : : :  
Db 2 HIRPG 6  
RESULT 45  
US-09-401-415-10  
; Sequence 10, Application US/09401415  
; Patent No. 6503732  
; GENERAL INFORMATION:  
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE  
; TITLE OF INVENTION: METHOD FOR USING TOBACCO MOSAIC VIRUS TO  
; OVERPRODUCE PEPTIDES AND PROTEINS  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Spensley Horn Jadas & Lubitz  
; STREET: 1880 Century Park East, Suite 500  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90067

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: US/09/401,415  
APPLICATION NUMBER: US/09/401,415  
FILING DATE: 21-Sep-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/01467  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Bostich, June M.  
REGISTRATION NUMBER: 31,238  
REFERENCE/DOCKET NUMBER: FD-4074  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..10  
SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-09-401-415-10

Query Match 36.6%; Score 26; DB 4; Length 10;  
Best Local Similarity 80.0%; Pred.No. 3.1e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 HYGP 10  
| | |  
Db 3 HIGPG 7

Search completed: August 30, 2004, 10:57:15  
Job time : 6.34797 secs



Db 1 NFKLKHYPGW 11

# RESULT 2

ID AAY69947 standard; peptide; 10 AA.

XX AAY69947;

DT 11-APR-2000 (first entry)

XX Human cyclophilin B peptide fragment #27.

DE Human cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;

KW HLA antigen; diagnosis; tumour; therapy.

XX Homo sapiens.

XX WO967288-A1.

PD 29-DEC-1999.

PF 24-JUN-1999; 99WO-JP003360.

PR 25-JUN-1998; 98JP-00178449.

XX (SUMU) SUMITOMO PHARM CO LTD.

PA (ITOH/) ITOH K.

PI Itoh K, Gomi S;

DR WPI; 2000-116932/10.

XX Tumor antigen peptides derived from cyclophilin B for treatment and

PT diagnosis of tumors.

XX Claim 4; Page 56; 64pp; Japanese.

CC This sequence represents a cyclophilin B peptide of the invention. The

CC peptides are tumour antigen peptides derived from cyclophilin B, that

CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The

CC peptides are used for the treatment and diagnosis of tumours

XX Sequence 10 AA;

QY 3 KKLKHYPGW 11

Db 1 KKLKHYPGW 9

Query Match 83.1%; Score 59; DB 3; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.0026;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AC ABR84352;

DT 06-NOV-2003 (first entry)

DE Human CYPB HLA-A2 epitope, SEQ ID NO:3.

KW Antigen specific T-cell; detection; diagnosis; cancer specific T-cell;

KW cancer; tumour; cervical cancer; prostate cancer; cellular immunity;

KW immune therapy; cytotoxic; immunostimulant; vaccine; antigenic peptide;

XX human; human leukocyte antigen; HLA-A2 epitope.

OS Homo sapiens.

XX JP2002365286-A.

PD 18-DEC-2002.

XX 18-SEP-2001; 2001JP-00283413.

PR 13-NOV-2000; 2000JP-00345094.

XX (ITOY/) ITO Y.

DR WPI; 2003-508315/48.

XX A detection method of antigen specific T-cells, comprises the use of

PT plural antigenic peptides, useful in semi-quantitative determination of

PT cancer specific T-cell frequencies and for monitoring cellular immunity.

XX Example 7; Page 8; 18pp; Japanese.

CC The invention relates to a method for the detection of antigen specific T

CC cells in a blood sample involving the use of a plurality of antigenic

CC peptides. The method comprises sampling of peripheral blood monocytes;

CC stimulation of the collected peripheral blood monocytes with antigens;

CC without direct use of antigen presenting cells; and detection of T-cells

CC specific to the antigen in the stimulated monocytes. The method is

CC particularly used for the detection of cancer as it can be used in semi-

CC quantitative determination of cancer specific T-cells. It can also be

CC used for cancer vaccine therapy for patients with cervical or prostate

CC cancer. The method can additionally be used to monitor of cellular

CC immunity and cancer immune therapy by detection of specific T-cell

CC frequencies. Sequences ABR84350-ABR84365 represent HLA-A2 (human

CC leukocyte antigen) peptides of human origin used in an example from the

XX invention

XX Sequence 10 AA;

QY 3 KKLKHYPGW 11

Db 1 KKLKHYPGW 9

Query Match 83.1%; Score 59; DB 6; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.0026;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AC AAY69928;

DT 11-APR-2000 (first entry)

DE Human cyclophilin B peptide fragment #8.

KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;

KW HLA antigen; diagnosis; tumour; therapy.

XX Homo sapiens.

XX WO967288-A1.

PD 29-DEC-1999.

PF 24-JUN-1999; 99WO-JP003360.

PR 25-JUN-1998; 98JP-00178449.

XX (SUMU) SUMITOMO PHARM CO LTD.

PA (ITOH/) ITOH K.

PI Itoh K, Gomi S;

DR WPI; 2000-116932/10.

XX Tumor antigen peptides derived from cyclophilin B for treatment and

PT diagnosis of tumors.  
XX  
PS Claim 4; Page 51; 64pp; Japanese.  
XX  
CC This sequence represents a cyclophilin B peptide of the invention. The  
CC peptides are tumor antigen peptides derived from cyclophilin B, that  
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The  
CC peptides are used for the treatment and diagnosis of tumors  
XX  
SQ Sequence 9 AA;  
Query Match 63.4%; Score 45; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 6 HYPGM 11  
1 HYPGM 6  
DB  
RESULT 5  
ABP74769  
ID ABP74769 standard; peptide; 14 AA.  
XX  
AC ABP74769;  
XX  
DT 03-FEB-2003 (first entry)  
XX  
DE Proteome analysis related peptide #54.  
XX  
KM Proteome analysis; isolation; determination; diagnostic assay; detection;  
KM protein marker; identification; metastatic; invasive cancer;  
KM differential expression; signalling pathway; chromatography.  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200277016-A2.  
XX  
XX 03-OCT-2002.  
XX  
PF 22-MAR-2002; 2002WO-EP003368.  
XX  
PR 22-MAR-2001; 2001US-0278171P.  
PR 12-SEP-2001; 2001US-0318748P.  
PR 20-SEP-2001; 2001US-0323939P.  
XX  
PA (VLAAS) VLAMS INTERNUNIVERSITAIR INST BIOTECHNOG.  
XX  
PI Vandekerckhove J, Gevaert K;  
XX  
DR WPI; 2003-067379/06.  
XX  
PT Method for isolation of peptides from complex mixture of peptides  
PT involves specific chemical and/or enzymatic alteration of at least one  
PT type of peptide.  
XX  
PS Example 20; Page 141; 193pp; English.  
XX  
CC The present invention describes a method (M1) for the isolation of a  
CC subset of peptides from a protein peptide mixture (P1). M1 involves: (a)  
CC separating the protein peptide mixture into fractions of peptides via  
CC chromatography; (b) chemically, or enzymatically, or chemically and  
CC enzymatically, altering at least one amino acid of at least one of the  
CC peptides in each fraction, thereby generating a subset of altered  
CC peptides; and (c) isolating the altered (flagged) peptides out of each  
CC fraction via chromatography, where the chromatography of steps (a) and  
CC (c) is performed with the same type of chromatography. M1 can be used for  
CC the isolation and determination of peptides from protein peptide  
CC mixtures. M1 can also be used in diagnostic assays for detection of the  
CC presence, the absence or a variation in expression level of at least one  
CC protein marker or a specific set of proteins indicative of a disease  
CC state. M1 can be used for identifying target proteins present in

CC metastatic and invasive cancers, in differential expression of proteins  
CC in transgenic mice, identification of proteins that are upregulated or  
CC down regulated in disease tissues, in identification of intracellular  
CC changes in cells with physiological changes such as metabolic shift, in  
CC the identification of biomarkers in cancers and in the identification of  
CC signalling pathways. The method is gel-free methodology for qualitative  
CC and quantitative proteome analysis without the need for multidimensional  
CC chromatography and without the use of affinity tags. ABP74714 to ABP75130  
CC represent peptide sequences used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 14 AA;  
Query Match 63.4%; Score 45; DB 6; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.89;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 6 HYPGM 11  
1 HYPGM 6  
DB  
RESULT 6  
AAR47787  
ID AAR47787 standard; protein; 14 AA.  
XX  
AC AAR47787;  
XX  
DT 25-MAR-2003 (revised)  
DT 27-JUL-1994 (first entry)  
XX  
DE HIV epitope #120.  
XX  
KM HIV-specific; principal neutralisation; epitope; antigen; conjugate;  
KM outer membrane proteosome; Neisseria; AIDS; vaccine; HIV; infection;  
KM disease; antibody; human; monoclonal antibody; 447 antibody.  
XX  
OS Human immunodeficiency virus.  
XX  
XX WO9402626-A1.  
XX  
XX 03-FEB-1994.  
XX  
PF 19-JUL-1993; 93WO-US006751.  
XX  
PR 20-JUL-1992; 92US-00917212.  
PR 20-JUL-1992; 92US-00917214.  
PR 20-JUL-1992; 92US-00917215.  
PR 20-JUL-1992; 92US-00917217.  
XX  
PA (MERI) MERCK & CO INC.  
XX  
PI Keller PM, Conley AJ, Shaw AR, Arnold BA;  
XX  
DR WPI; 1994-04884/06.  
XX  
PT New conjugates for treating or preventing HIV infection - comprising HIV-  
PT specific neutralisation epitopes covalently linked to outer membrane  
PT proteosome of Neisseria.  
XX  
PS Claim 1; Page 151; 181pp; English.  
XX  
CC The sequences given in AAR47668-788 are HIV-specific selected principal  
CC neutralisation epitopes which may be used in an antigenic conjugate  
CC linked to purified outer membrane proteosome of Neisseria. This conjugate  
CC may be used in an AIDS vaccine which may be used pre- and post-exposure  
CC to prevent or treat HIV infection or disease. The vaccine is capable of  
CC eliciting specific HIV neutralising antibodies and bind the broadly  
CC neutralising human monoclonal antibody (447 antibody). (Updated on 25-MAR  
CC -2003 to correct PN field.)  
XX  
SQ Sequence 14 AA;

Query Match 52.1%; Score 37; DB 2; Length 14;  
Best Local Similarity 55.6%; Pred. No. 20;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 FKLKHYGP 10  
Db 3 YRAAHYGP 11

RESULT 7  
AAV98453  
ID AAV98453 standard; peptide; 13 AA.

AC AAV98453;

DT 31-JUL-2000 (first entry)

DE Alpha D peptide derived from TrkB SEQ ID NO:168.

XX Alpha D peptide; Alpha D region; protein kinase; modulation; activity;  
XX cytosolic; anti-diabetic; anorectic; antiinflammatory; dermatological;  
XX immunosuppressive; immunomodulator; osteopathic; cardiac; vasotropic;  
XX antiarteriosclerotic; protein kinase modulator; cancer; proliferation;  
XX restenosis; atherosclerosis; skin disorder; diabetes; obesity;  
XX central nervous system disorder; inflammatory disorder; osteoporosis;  
XX autoimmune disease; immune disorder; cardiovascular disease.

OS Homo sapiens.

PN WO200018895-A1.

PD 06-APR-2000.

PF 24-SEP-1999; 99WO-US022106.

PR 25-SEP-1998; 98US-00161094.

XX (CHIL-) CHILDRENS MEDICAL CENT.

PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.

PI Ben-Sasson SA;

DR WPI; 2000-328722/28.

PT Peptide derivatives of protein kinase alpha D regions which selectively  
modulate the activity of protein kinases.

PS Claim 23; Fig 3; 148bp; English.

XX The present invention describes a peptide derivative (A) of the protein  
XX kinase alpha D region comprising 5-30 amino acids, which modulates the  
XX activity of the protein kinase. AAV98286 to AAV98455 represent peptides  
XX derived from protein kinase alpha D regions, which are used in the  
XX exemplification of the present invention. The peptides have cytosolic,  
XX anti-diabetic, anorectic, antiinflammatory, dermatological, cardiac,  
XX immunosuppressive, immunomodulator, osteopathic, vasotropic and  
XX antiarteriosclerotic activities, and are protein kinase modulators. The  
XX peptides can be used as test peptides to identify protein kinase  
XX modulators. They can also be used to modulate the activity of a protein  
XX kinase in a subject, and in a method of detecting a ligand that binds to  
XX the alpha D region of a protein kinase. They may be used to produce  
XX antibodies that bind to the alpha D region of a protein kinase. The  
XX peptides are useful in the treatment of diseases caused by over- or under  
XX -activity of a protein kinase, e.g. cancer, diseases caused by  
XX proliferation of smooth muscle (e.g. restenosis and atherosclerosis),  
XX skin disorders, diabetes, obesity, diseases of the central nervous  
XX system, inflammatory disorders, autoimmune diseases and other immune  
XX disorders, osteoporosis and cardiovascular diseases

SQ Sequence 13 AA;

Query Match 50.7%; Score 36; DB 3; Length 13;  
Best Local Similarity 66.7%; Pred. No. 28;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 NFKLKHYP 9  
Db 3 NFKLRAHYP 11

RESULT 8  
AAR47734  
ID AAR47734 standard; protein; 14 AA.

AC AAR47734;

DT 25-MAR-2003 (revised)

DT 27-JUL-1994 (first entry)

DE HIV epitope #67.

XX HIV-specific; principal neutralisation; epitope; antigen; conjugate;  
XX outer membrane proteosome; Neisseria; AIDS; vaccine; HIV; infection;  
XX disease; antibody; human; monoclonal antibody; 447 antibody.

OS Human immunodeficiency virus.

PN WO9402626-A1.

PD 03-FEB-1994.

PF 19-JUL-1993; 93WO-US006751.

PR 20-JUL-1992; 92US-00917212.

PR 20-JUL-1992; 92US-00917214.

PR 20-JUL-1992; 92US-00917215.

PR 20-JUL-1992; 92US-00917217.

XX (MERI) MERCK & CO INC.

PI Keller PM, Conley AJ, Shaw AR, Arnold BA;

DR WPI; 1994-048884/06.

PT New conjugates for treating or preventing HIV infection - comprising HIV-  
PT specific neutralisation epitopes covalently linked to outer membrane  
PT proteosome of Neisseria.

PS Claim 1; Page 125; 181pp; English.

XX The sequences given in AAR47668-768 are HIV-specific selected principal  
XX neutralisation epitopes which may be used in an antigenic conjugate  
XX linked to purified outer membrane proteosome of Neisseria. This conjugate  
XX may be used in an AIDS vaccine which may be used pre- and post-exposure  
XX to prevent or treat HIV infection or disease. The vaccine is capable of  
XX eliciting specific HIV neutralising antibodies and bind the broadly  
XX neutralising human monoclonal antibody (447 antibody). (Updated on 25-MAR  
XX -2003 to correct PN field.)

XX Sequence 14 AA;

Query Match 45.1%; Score 32; DB 2; Length 14;  
Best Local Similarity 71.4%; Pred. No. 1.5e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 KKLKHYGP 9  
Db 1 KANHYGP 7

RESULT 9  
AAV57711  
ID AAV57711 standard; peptide; 14 AA.

AC AAV57711;

XX



DT 14-MAR-2000 (first entry)  
 XX Rat clusterin 47 kDa peptide.  
 DE  
 XX Clusterin; immunosuppressant; organ rejection; tissue transplantation;  
 XX autoimmune disease; inflammatory disease; rheumatism; atopy;  
 KM systemic erythematosis; allergy; hay fever.  
 KM  
 XX Rattus sp.  
 OS  
 XX WO9962541-A1.  
 PN  
 XX 09-DEC-1999.  
 XX  
 PD 13-MAY-1999; 99WO-JP002474.  
 XX  
 PF 01-JUN-1998; 98JP-00151570.  
 XX  
 PR (HISM) HISAMITSU PHARM CO LTD.  
 XX  
 PA Yuda K, Akiyama K, Goto T, Goto S;  
 XX  
 PI WPI; 2000-072735/06.  
 XX  
 DR Immunosuppressants with reduced side-effects, useful for preventing  
 PT rejection in organ and tissue transplant and as remedies for autoimmune  
 PT diseases and inflammatory diseases (claimed) e.g. allergy.  
 PS  
 XX Example 3; Page 12; 28pp; Japanese.  
 XX  
 CC The present invention describes an immunosuppressant which contains a  
 CC clusterin. The present sequence represents a rat clusterin peptide from  
 CC an example of the present invention. Also described is a method for  
 CC treating rejection in organ and tissue transplant, autoimmune diseases or  
 CC inflammatory diseases by administering an effective dose of the  
 CC immunosuppressant. The immunosuppressant are useful for preventing  
 CC rejection in organ and tissue transplant, particularly of heart, liver,  
 CC lung, pancreas, kidney, small intestine, skin and bone marrow, and as  
 CC remedies for autoimmune diseases such as rheumatism, atopy, systemic  
 CC erythematosis, and inflammatory diseases including allergy such as hay  
 CC fever. The drugs are efficacious, with little side-effects  
 CC  
 SQ Sequence 14 AA:  
 Query Match 45.1%; Score 32; DB 3; Length 14;  
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 4 LKHGCP 9  
 | | | | |  
 DB 5 LSHYGP 10  
 RESULT 10  
 AAR88101  
 ID AAR88101 standard; peptide; 8 AA.  
 XX  
 AC AAR88101;  
 XX  
 DT 22-JUL-1996 (first entry)  
 XX  
 DE Bovine p32 11-cis-retinol dehydrogenase tryptic fragment P322.  
 XX  
 KM Clone p-lambda-321; bovine; p32; 11-cis-retinol; dehydrogenase;  
 KM 11-cis-retinaldehyde; diagnosis; retinoid; retinitis pigmentosa;  
 KM psoriasis; acne; cancer; T-cell leukaemia; drug development; treatment;  
 KM retinal pigment epithelial cell; tryptic fragment; leukemia.  
 KM  
 XX Synthetic.  
 OS  
 XX WO9534580-A1.  
 PN  
 XX 21-DEC-1995.

XX 06-JUN-1995; 95WO-US006256.  
 PF  
 XX 10-JUN-1994; 94US-00258418.  
 PR  
 XX 20-JUN-1995; 95US-00375962.  
 XX  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 XX  
 PI Hellman U, Wernstedt C, Eriksson U;  
 XX  
 DR WPI; 1996-049624/05.  
 XX  
 PT Nucleic acid encoding a retinol dehydrogenase protein - used to develop  
 PT prods. for the diagnosis and treatment of retinoid-linked pathological  
 PT conditions.  
 PS  
 XX Example 4; Page 10; 35pp; English.  
 XX  
 CC Bovine p32 11-cis-retinol dehydrogenase, which catalyses the conversion  
 CC of 11-cis-retinol into 11-cis-retinaldehyde, can be used for the  
 CC diagnosis of retinoid linked pathological conditions, e.g. retinitis  
 CC pigmentosa, psoriasis, acne and certain cancers (i.e. T-cell leukaemias),  
 CC and for the development of drugs to treat these conditions. The p32 DNA  
 CC clone p-lambda-321 was isolated from bovine retinal pigment epithelial  
 CC (RPE) cell mRNA, using degenerate primers based on the 32 kD bovine RPE  
 CC cell derived protein p32 tryptic fragments AAR8100-04  
 CC  
 SQ Sequence 8 AA:  
 Query Match 43.7%; Score 31; DB 2; Length 8;  
 Best Local Similarity 80.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 7 YGRCW 11  
 | | | | |  
 DB 1 YSPCW 5  
 RESULT 11  
 AAM18339  
 ID AAM18339 standard; peptide; 8 AA.  
 XX  
 AC AAM18339;  
 XX  
 DT 18-AUG-1997 (first entry)  
 XX  
 DE Bovine p32 11-cis-retinol dehydrogenase tryptic peptide p322.  
 XX  
 KM 11-Cis retinol dehydrogenase; p32; 11-cis retinaldehyde;  
 KM retinitis pigmentosa; psoriasis; acne; cancer; diagnosis; therapy.  
 KM  
 XX Bos taurus.  
 OS  
 XX WO9719167-A1.  
 PN  
 XX 29-MAY-1997.  
 PD  
 XX 14-NOV-1996; 96WO-US018295.  
 PF  
 XX 22-NOV-1995; 95US-00562114.  
 PR  
 XX 11-OCT-1996; 96US-00729594.  
 XX  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 XX  
 PI Eriksson U, Simon A, Romert A;  
 XX  
 DR WPI; 1997-298106/27.  
 XX  
 PT New 11-cis retinol dehydrogenase gene - used to develop products for the  
 PT diagnosis and therapy of conditions such as retinitis pigmentosa,  
 PT psoriasis and cancers.  
 PS  
 XX Example 4; Page 11; 68pp; English.

XX Tryptic peptides (AAW18338-42) were isolated from bovine retinal pigment  
 CC epithelial (RPE) membrane protein p32. PCR primers (see also AAT68946-49)  
 CC based on these primers were used to amplify cDNA (see also AAT68935)  
 CC coding for bovine p32 (AAW18343) from a RPE cDNA library. Peptide p322  
 CC corresponds to amino acids 281-288 of the p32 sequence deduced from the  
 CC cDNA clone. p32 is an 11-cis retinol dehydrogenase and forms a complex  
 CC with a component of the membrane receptor for retinol binding protein  
 SQ Sequence 8 AA;

Query Match 43.7%; Score 31; DB 2; Length 8;  
 Best Local Similarity 80.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 YGPGW 11  
 DB 1 YSPGW 5

## RESULT 12

AAV01990  
 ID AAV01990 standard; peptide; 8 AA.

AC AAV01990;

DT 02-JUL-1999 (first entry)

DE Tryptic peptide of bovine p32 protein.

KM p32 protein; retinol dehydrogenase; 9-cis; 11-cis; 13-cis;  
 KM trans retinol dehydrogenase; oligomeric protein complex;  
 KM membrane receptor; retinol binding protein;  
 KM short chain alcohol dehydrogenase family; retinaldehyde;  
 KM retinitis pigmentosa; skin disorder; psoriasis; acne; T-cell leukemia.

OS Bos sp.

PN WO9916788-A1.

PD 08-APR-1999.

PF 21-SEP-1999; 98WO-US019836.

PR 26-SEP-1997; 97US-00937993.

PA (LUDWIG) LUDWIG INST CANCER RES.

PI Eriksson U, Simon A, Romert A;

DR WPI; 1999-255059/21.

PT New retinol dehydrogenase proteins, used to screen potential retinoid  
 PT drugs for treatment of various diseases, e.g. retinitis pigmentosa.

PS Example 4; Page 14; 88pp; English.

CC AAV01999-93 represent peptide obtained after tryptic digest of a p32  
 CC protein, isolated in the course of the invention. The specification  
 CC describes proteins having retinol dehydrogenase activity, such as 9-cis,  
 CC 11-cis, 13-cis, or trans retinol dehydrogenase activity. These proteins  
 CC form oligomeric protein complexes with the components of the membrane  
 CC receptor for retinol binding protein. The retinol dehydrogenase proteins  
 CC are members of the short chain alcohol dehydrogenase family. The  
 CC recombinant enzymes can be used to produce 9-cis and 11-cis  
 CC retinaldehydes. The proteins and nucleic acids encoding them can be used  
 CC to screen potential retinoid drugs for treatment of various diseases,  
 CC e.g. diseases of the eye such as retinitis pigmentosa and skin disorders  
 CC such as psoriasis and acne. Certain T-cell leukemias may also be tested  
 CC by retinoid drugs. Antibodies against the protein can be used to monitor  
 CC pathological conditions characterized by aberrant levels of a receptor  
 CC for retinol binding protein

SQ Sequence 8 AA;

Query Match 43.7%; Score 31; DB 2; Length 8;  
 Best Local Similarity 80.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 YGPGW 11  
 DB 1 YSPGW 5

## RESULT 13

AAR31264  
 ID AAR31264 standard; peptide; 9 AA.

AC AAR31264;

DT 12-FEB-1993 (first entry)

DE HIV principal determinant peptide.

KM AIDS; ARC; human immunodeficiency virus; vaccine; cyclic; Neisseria;  
 KM meningitidis b; outer membrane protein complex; OMPC; CPND23.

OS Synthetic.

PH Key Location/Qualifiers

FT Modified-site 1 /label= Nle

FT Modified-site 2 /note= "this position is linked to the OMPC of the

FT Modified-site 2 /note= "epsilon-amino group is condensed with C-terminal

FT Modified-site 9 /note= "forms amide bond with epsilon-amino of Lys(2) to

FT Modified-site 9 /note= "forms amide bond with epsilon-amino of Lys(2) to

PN EP467700-A.

PD 22-JAN-1992.

PF 19-JUL-1991; 91BP-00306598.

PR 19-JUL-1990; 90US-00555339.

PR 19-JUL-1990; 90US-00555966.

PR 19-JUN-1991; 91US-00715276.

PR 19-JUN-1991; 91US-00715278.

PA (MERI) MERCK & CO INC.

PI Leanza WJ, Marburg S, Tolman RL, Emini EA;

DR WPI; 1992-026505/04.

PT Conjugate proteins comprising HIV peptide components - useful for

PT preparing vaccines for e.g. AIDS or for treating infections.

PS Claim 12; Page 54; 63pp; English.

CC The invention relates to a co-conjugate comprising an immunogenic protein  
 CC or protein complex having a first set of covalent linkages to low  
 CC molecular weight moieties which have an anionic or polyanionic character  
 CC at physiological pH, and a second set of covalent linkages to peptides  
 CC comprising HIV principal neutralizing determinants (PND's) or  
 CC immunologically equivalent peptides. Preferably at least one set of the  
 CC covalent linkages is comprised of maleimide derivatives; the  
 CC (poly)anionic moiety is composed of one to five residues of the anionic  
 CC form of a carboxylic, sulphonic or phosphonic acid; the immunogenic  
 CC protein is the outer membrane protein complex (OMPC) of Neisseria  
 CC meningitidis b; and the PND peptide has a linear structure, a disulphide-  
 CC bonded cyclic structure, an amide-bonded cyclic structure or a thioether-  
 CC bonded cyclic structure. The present sequence (CPND23) is an example of a

CC PND peptide component used in the co-conjugate. The co-conjugate is  
 CC useful for inducing anti-peptide immune response in mammals, for inducing  
 CC HIV-neutralizing antibodies in mammals, for formulating vaccines to  
 CC prevent HIV infection or disease, including AIDS, or for treating humans  
 CC afflicted with HIV infection or disease  
 XX  
 SQ Sequence 9 AA;

Query Match 43.7%; Score 31; DB 2; Length 9;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 KHYPG 10  
 |||||  
 DB 2 KHIGPG 7

RESULT 14  
 AAR31301  
 ID AAR31301 standard; peptide; 9 AA.

AC AAR31301;  
 DT 11-FEB-1993 (first entry)

DE Cyclic HIV principal neutralizing determinant peptide.

XX Human immunodeficiency virus; PND; cyclic; conjugate; AIDS; ARC; vaccine;  
 KW immunogen; ELISA; analysis; cPND23.

OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /label= Nle

FT /note= "Z-Nle"

FT Modified-site 2 /note= "forms cyclic lactam bond, via epsilon-NH2, with C

FT /note= "terminal COOH"

FT Modified-site 9 /note= "forms cyclic amide bond with epsilon-NH2 of

PN EP471453-A.

PD 19-FEB-1992.

XX 19-JUL-1991; 91EP-00306582.

PR 19-JUL-1990; 90US-00555112.

XX (MERI ) MERCK & CO INC.

PI Suggs EE, Dolan CA, Bednarek MA, Tolman RL, Christensen BG;

DR WPI; 1992-058511/08.

PT New cyclic HIV principal neutralising determinant peptide(s) - used as

XX laboratory tools and as vaccines against HIV, AIDS, arc etc.

PS Claim 4; Page 21; 25pp; English.

XX The peptide (cPND23) is a specifically claimed example of HIV principal

CC neutralizing determinant peptides which are covered generically in Claims

CC 1-3 (AAR31291, AAR31292), the peptides being stably cyclised as a result

CC of a lactam bridge between an NH2 on the N-terminal side of the loop

CC amino acids and a COOH on the C-terminal side of the loop amino acids.

CC The bond is less labile than a disulphide bond. The stable cyclic HIV PND

CC peptides (cPND's) may be used as analytical tools and as reagents in

CC ELISA assays. They may also be conjugated to an immunogenic carrier (a

CC protein and/or a polysaccharide; e.g. PRP or OMP) to give a product

CC useful for inducing mammalian anti-peptide, anti-HIV, or HIV-neutralizing

CC immune responses and for formulating vaccines to prevent HIV disease,

CC including AIDS and ARC, or for treating humans afflicted with HIV disease  
 CC such as AIDS or ARC  
 XX  
 SQ Sequence 9 AA;

Query Match 43.7%; Score 31; DB 2; Length 9;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 KHYPG 10  
 |||||  
 DB 2 KHIGPG 7

RESULT 15  
 AAR26700  
 ID AAR26700 standard; peptide; 9 AA.

AC AAR26700;  
 DT 09-FEB-1993 (first entry)

DE HIV-PND-polysaccharide-protein conjugate vaccine.

XX Human immunodeficiency virus; principal neutralizing determinant;  
 KW outer membrane protein complex; OMP; Neisseria; AIDS; cyclic; cPND23.

OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /label= Nle

FT /note= "bonded via N-terminal to polysaccharide- protein

FT Modified-site 2 /note= "epsilon-amino forms cyclic peptide with C-

FT Modified-site 9 /note= "condenses with side chain NH2 of Lys(2) to give

FT /note= "cyclic peptide"

PN EP468714-A.

PD 29-JAN-1992.

XX 19-JUL-1990; 90US-00555558.

PR 19-JUL-1990; 90US-00555558.

PR 19-JUN-1991; 91US-00715275.

XX 19-JUN-1991; 91US-00715277.

XX (MERI ) MERCK & CO INC.

PI Marburg S, Tolman RL, Emili EA;

DR WPI; 1992-034437/05.

PT HIV peptide-polysaccharide-protein conjugates - used in vaccines or to

XX produce antibodies to prevent or treat HIV infection.

PS Claim 9; Page 55; 63pp; English.

XX The invention relates to a conjugate of an HIV principal neutralizing

CC determinant (PND), or an immunologically equivalent peptide (PRP),

CC covalently coupled to an immunogenic protein or protein complex through

CC an antigenic polysaccharide linker. Pref. the immunogenic protein is the

CC outer membrane protein complex (OMP) of Neisseria meningitidis b and the

CC PND peptide has a linear structure, a disulphide-bonded cyclic structure,

CC an amide-bonded cyclic structure or a thioether-bonded cyclic structure.

CC The present sequence (cPND23) is an example of a PND peptide component.

CC The conjugates are used for inducing HIV-neutralising antibodies or for

CC making vaccines to prevent contraction of HIV infection or disease. The

CC antiobodies can be used for passively protecting against infection by HIV,  
 CC or for protecting against proliferation of HIV post-infection, or for  
 CC treating AIDS, or in diagnostic assays  
 XX  
 SQ Sequence 9 AA;

Query Match 43.7%; Score 31; DB 2; Length 9;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHGPG 10  
 DB 2 KHGPG 7

RESULT 16  
 AAM03401

ID AAM03401 standard; peptide; 9 AA.

AC AAM03401;

DT 07-OCT-1996 (first entry)

DE HIV principal neutralizing determinant CPND815.

DE conjugate; PND; HIV; principal neutralizing determinant; OMPC;

KM outer membrane protein complex; anionic spacer; vaccine;

XX human immunodeficiency virus; water-soluble.

OS Synthetic.

Key Location/Qualifiers

Modified-site 1

/label= Nle

/note= "the N-terminal of this norleucine residue is  
 linked to Neisseria meningitidis OMPC via a specified  
 anionic spacer group"

Modified-site 2

/label= cycle

/note= "the epsilon-amino of this residue forms a peptide  
 bond with the terminal carboxy group of Ala(9), giving a  
 cyclic peptide"

Modified-site 9  
 /note= "the carboxy group is condensed onto the epsilon-  
 amino of Lys(2). See above"

GB227195-A.

04-MAY-1994.

12-OCT-1993; 93GB-00020943.

15-OCT-1992; 92US-00963327.

(MERI) MERCK & CO INC.

Tolman RL, Marburg S, Leanza WL, Lombardo VK;

WPI, 1994-128412/16.

New conjugates of outer membrane protein and HIV epitope - for generating  
 HIV-neutralizing response, have components joined by anionic spacer to  
 ensure solubility of prod.

Claim 6; Page 68; 73pp; English.

A new conjugate immunogen comprises (a) the OMPC of Neisseria  
 meningitidis b as a protein carrier (b) a principal neutralizing  
 determinant (PND) of HIV as a peptide; (c) an anionic spacer linking (a)  
 and (b). The conjugate is water-soluble, yet can carry a high peptide  
 epitope loading. It is useful as a vaccine against HIV. The present  
 sequence is an example of a PND used in the conjugate

XX  
 SQ Sequence 9 AA;

Query Match 43.7%; Score 31; DB 2; Length 9;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHGPG 10  
 DB 2 KHGPG 7

RESULT 17  
 AAR31271

ID AAR31271 standard; peptide; 10 AA.

AC AAR31271;

DT 12-FEB-1993 (first entry)

DE HIV principal determinant peptide.

KM AIDS; ARC; human immunodeficiency virus; vaccine; cyclic; Neisseria;

XX meningitidis b; outer membrane protein complex; OMPC; CPND30.

OS Synthetic.

Key Location/Qualifiers

Modified-site 1

/label= Nle

/note= "this position is linked to the OMPC of the  
 conjugate"

Modified-site 10

/note= "epsilon-amino group is condensed with C-terminal  
 COOH to form cyclic peptide"

/note= "forms amide bond with epsilon-amino of Lys(2) to  
 give cyclic molecule"

EP467700-A.

22-JAN-1992.

19-JUL-1991; 91EP-00306598.

19-JUL-1990; 90US-00555332.

19-JUL-1990; 90US-00555966.

19-JUN-1991; 91US-00715276.

19-JUN-1991; 91US-00715278.

(MERI) MERCK & CO INC.

Leanza WL, Marburg S, Tolman RL, Emini BA;

WPI, 1992-026505/04.

Conjugate proteins comprising HIV peptide components - useful for  
 preparing vaccines for e.g. AIDS or for treating infections.

Claim 12; Page 55; 63pp; English.

The invention relates to a co-conjugate comprising an immunogenic protein  
 or protein complex having a first set of covalent linkages to low  
 molecular weight moieties which have an anionic or polyanionic character  
 at physiological pH, and a second set of covalent linkages to peptides  
 comprising HIV principal neutralizing determinants (PNDs) or  
 immunologically equivalent peptides. Preferably at least one set of the  
 covalent linkages is comprised of maleimide derivatives; the  
 (poly)anionic moiety is composed of one to five residues of the anionic  
 form of a carboxylic, sulphonic or phosphonic acid; the immunogenic  
 protein is the outer membrane protein complex (OMPC) of Neisseria  
 meningitidis b; and the PND peptide has a linear structure, a disulphide-  
 bonded cyclic structure, an amide-bonded cyclic structure or a thioether-



CC The invention relates to a co-conjugate comprising an immunogenic protein  
 CC or protein complex having a first set of covalent linkages to low  
 CC molecular weight moieties which have an anionic or polyanionic character  
 CC at physiological pH, and a second set of covalent linkages to peptides  
 CC comprising HIV principal neutralizing determinants (PND's) or  
 CC immunologically equivalent peptides. Preferably at least one set of the  
 CC covalent linkages is comprised of maleimide derivatives; the  
 CC (poly)anionic moiety is composed of one to five residues of the anionic  
 CC form of a carboxylic, sulphonic or phosphonic acid; the immunogenic  
 CC protein is the outer membrane protein complex (OMP) of *Neisseria*  
 CC meningitidis b, and the PND peptide has a linear structure, a disulphide-  
 CC bonded cyclic structure, an amide-bonded cyclic structure or a thioether-  
 CC bonded cyclic structure. The present sequence (CPND27) is an example of a  
 CC PND peptide component used in the co-conjugate. The co-conjugate is  
 CC useful for inducing anti-peptide immune response in mammals, for inducing  
 CC HIV-neutralizing antibodies in mammals, for formulating vaccines to  
 CC prevent HIV infection or disease, including AIDS, or for treating humans  
 CC afflicted with HIV infection or disease

Sequence 10 AA;

Query Match 43.7%; Score 31; DB 2; Length 10;  
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHVPG 10  
 Db 2 KHVPG 7

RESULT 20

AAR31272  
 ID AAR31272 standard; peptide; 10 AA.

AAR31272;

12-FEB-1993 (first entry)

HIV principal determinant peptide.

AIDS; ARC; human immunodeficiency virus; vaccine; cyclic; *Neisseria*;  
 meningitidis b; outer membrane protein complex; OMP; CPND31.

Synthetic.

Key Location/Qualifiers

Modified-site 1  
 /note= "N(epsilon)-substituted by Nle, which in turn is  
 bonded to the OMP of the conjugate; and N(alpha)-  
 condensed by side-chain COOH of Glu(10) to form a cyclic  
 molecule"

Modified-site 10  
 /note= "Glu-NH2; and omega-COOH condenses with the alpha-  
 amino group of Lys(1), giving cyclic peptide"

EP467700-A.

22-JAN-1992.

19-JUL-1991; 91EP-00306598.

19-JUL-1990; 90US-00555339.

19-JUL-1990; 90US-00555966.

19-JUN-1991; 91US-00715276.

19-JUN-1991; 91US-00715278.

(MERI ) MERCK & CO INC.

Leanza WJ, Marburg S, Tolman RL, Emini EA;  
 WPI; 1992-026505/04.  
 Conjugate proteins comprising HIV peptide components - useful for

PT preparing vaccines for e.g. AIDS or for treating infections.

PS Claim 12; Page 55; 63pp; English.

CC The invention relates to a co-conjugate comprising an immunogenic protein  
 CC or protein complex having a first set of covalent linkages to low  
 CC molecular weight moieties which have an anionic or polyanionic character  
 CC at physiological pH, and a second set of covalent linkages to peptides  
 CC comprising HIV principal neutralizing determinants (PND's) or  
 CC immunologically equivalent peptides. Preferably at least one set of the  
 CC covalent linkages is comprised of maleimide derivatives; the  
 CC (poly)anionic moiety is composed of one to five residues of the anionic  
 CC form of a carboxylic, sulphonic or phosphonic acid; the immunogenic  
 CC protein is the outer membrane protein complex (OMP) of *Neisseria*  
 CC meningitidis b; and the PND peptide has a linear structure, a disulphide-  
 CC bonded cyclic structure, an amide-bonded cyclic structure or a thioether-  
 CC bonded cyclic structure. The present sequence (CPND31) is an example of a  
 CC PND peptide component used in the co-conjugate. The co-conjugate is  
 CC useful for inducing anti-peptide immune response in mammals, for inducing  
 CC HIV-neutralizing antibodies in mammals, for formulating vaccines to  
 CC prevent HIV infection or disease, including AIDS, or for treating humans  
 CC afflicted with HIV infection or disease

Sequence 10 AA;

Query Match 43.7%; Score 31; DB 2; Length 10;  
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHVPG 10  
 Db 1 KHVPG 6

RESULT 21

AAR31256  
 ID AAR31256 standard; peptide; 10 AA.

AAR31256;

12-FEB-1993 (first entry)

HIV principal determinant peptide.

AIDS; ARC; human immunodeficiency virus; vaccine; cyclic; *Neisseria*;  
 meningitidis b; outer membrane protein complex; OMP; CPND8.

Synthetic.

Key Location/Qualifiers

Modified-site 1  
 /label= Nle  
 /note= "this position is linked to the OMP of the  
 conjugate"

Modified-site 2  
 /note= "epsilon-amino group is condensed with C-terminal  
 COOH to form cyclic peptide"  
 10  
 /note= "forms amide bond with epsilon-amino of Lys(2) to  
 give cyclic molecule"

EP467700-A.

22-JAN-1992.

19-JUL-1991; 91EP-00306598.

19-JUL-1990; 90US-00555339.

19-JUL-1990; 90US-00555966.

19-JUN-1991; 91US-00715276.  
 19-JUN-1991; 91US-00715278.  
 (MERI ) MERCK & CO INC.

XX	Leanza WJ, Marburg S, Tolman RL, Emini EA;
XX	WPI, 1992-026505/04.
DR	
PT	Conjugate proteins comprising HIV peptide components - useful for
XX	preparing vaccines for e.g. AIDS or for treating infections.
XX	
PS	Claim 12; Page 53; 63pp; English.
XX	
CC	The invention relates to a co-conjugate comprising an immunogenic protein
CC	or protein complex having a first set of covalent linkages to low
CC	molecular weight moieties which have an anionic or polyanionic character
CC	at physiological pH, and a second set of covalent linkages to peptides
CC	comprising HIV principal neutralizing determinants (PND's) or
CC	immunologically equivalent peptides. Preferably at least one set of the
CC	covalent linkages is comprised of maleimide derivatives; the
CC	(poly)anionic moiety is composed of one to five residues of the anionic
CC	form of a carboxylic, sulphonic or phosphonic acid; the immunogenic
CC	protein is a dimeric protein complex (OMPC) of Neisseria
CC	meningitidis b; and the PND peptide has a linear structure, a disulphide-
CC	bonded cyclic structure, an amide-bonded cyclic structure or a thioether-
CC	bonded cyclic structure. The present sequence (CPND8) is an example of a
CC	PND peptide component used in the co-conjugate. The co-conjugate is
CC	useful for inducing anti-peptide immune response in mammals, for inducing
CC	HIV-neutralizing antibodies in mammals, for formulating vaccines to
CC	prevent HIV infection or disease, including AIDS, or for treating humans
CC	afflicted with HIV infection or disease
XX	
SO	Sequence 10 AA:
QY	Query Match 43.7%; Score 31; DB 2; Length 10;
DB	Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches	5; Conservative 0; Mismatches 1; Indels 0; Gaps 0.
5	KHYGPG 10
2	KHIGPG 7
XX	
RESULT 22	
AA30018	
ID	AA30018 standard; peptide; 10 AA.
XX	
AC	AA30018;
XX	
DT	25-MAR-2003 (revised)
DT	28-APR-1993 (first entry)
XX	
DE	HIV CPND31.
XX	
KW	Human immunodeficiency virus; AIDS; PND; MIEP; conjugate;
KW	major immune enhancing protein; vaccine; anti-HIV antibodies; immunogen;
KW	passive immunisation; principle neutralising determinant.
XX	
OS	Human immunodeficiency virus.
XX	
PH	Key
FT	Modified-site 1 Location/Qualifiers
FT	Modified-site 2.10 /label= N1e
FT	Modified-site /note= "Lys-NH-NH-CO(CH2)2-CH(CONH2)-NH-CO-Phe"
XX	
PN	EP519554-A1.
XX	
PD	23-DEC-1992.
XX	
PF	11-JUN-1992; 92EP-00201693.
XX	
PR	19-JUN-1991; 91US-00715273.
XX	
PA	(MERT) MERCK & CO INC.
XX	

PI Emami A, Liu MA, Wardburg S, Tolman RL;  
 DR WPI, 1992-425771/52.  
 XX  
 PT Conjugates of HIV-1 PND peptide(s) with the MIEP of *Neisseria*  
 XX meningitidis - useful as a vaccine for treating and preventing HIV-1  
 PT infection, e.g. AIDS in humans.  
 XX  
 PS Claim 9; Page 60; 66pp; English.  
 XX  
 CC The peptide is HIV principle neutralising determinant CPND31 and is used  
 CC as part of a conjugate comprising the major immune enhancing protein  
 CC (MIEP) of *Neisseria meningitidis* covalently linked to the HIV PND. The  
 CC conjugate may be used to prepare vaccines against HIV infections, e.g.  
 CC AIDS, as research tools for studying PND structure- function  
 CC relationships, or as immunogens for use in the passive immunisation of  
 CC humans. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 10 AA;  
 QY Query Match 43.7%; Score 31; DB 2; Length 10;  
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0.  
 OY 5 KHVPG 10  
 |||||  
 Db 2 KHIGPG 7  
 RESULT 23  
 AAR31309  
 ID AAR31309 standard; peptide; 10 AA.  
 XX AAR31309;  
 AC  
 XX 11-FEB-1993 (first entry)  
 DT  
 XX  
 DE Cyclic HIV principal neutralising determinant peptide.  
 XX  
 KM Human immunodeficiency virus; PND; cyclic; conjugate; AIDS; ARC; vaccine;  
 XX immunogen; ELISA; analysis; CPND31.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1  
 FT /note= "N(epsilon)-acylated by H-Nle, N(alpha) condensed  
 FT with side-chain COOH of C-terminal Glu to form cyclic  
 FT molecule"  
 FT Modified-site 10  
 FT /note= "Glu-NH2; omega-COOH forms cyclic amide bond with  
 FT alpha-NH2 of Lys(1)"  
 FT  
 XX  
 PN EP471453-A.  
 XX  
 PD 19-FEB-1992.  
 XX  
 PF 19-JUL-1991; 91EP-00306582.  
 XX  
 PR 19-JUL-1990; 90US-0055112.  
 XX  
 PA (MERI ) MERCK & CO INC.  
 XX  
 PI Sugg EE, Dolan CA, Bednarek MA, Tolman RL, Christense BG;  
 DR WPI, 1992-058511/08.  
 XX  
 PT New cyclic HIV principal neutralising determinant peptide(s) - used as  
 PT laboratory tools and as vaccines against HIV, AIDS, arc etc.  
 XX  
 PS Claim 4; Page 22; 25pp; English.  
 XX  
 CC The peptide (CPND31) is a specifically claimed example of HIV principal

neutralizing determinant peptides which are covered generically in Claims 1-3 (AAR11291, AAR11292). The peptides being stably cyclised as a result of a lactam bridge between an NH2 on the N-terminal side of the loop amino acids and a COOH on the C-terminal side of the loop amino acids. The bond is less labile than a disulphide bond. The stable cyclic HIV PND peptides (cPND's) may be used as analytical tools and as reagents in ELISA assays. They may also be conjugated to an immunogenic carrier (a protein and/or a polysaccharide; e.g. PAP or OMP) to give a product useful for inducing mammalian anti-peptide, anti-HIV, or HIV-neutralizing immune responses and for formulating vaccines to prevent HIV disease, including AIDS and ARC, or for treating humans afflicted with HIV disease such as AIDS or ARC

CC loop amino acids and a COOH on the C-terminal side of the loop amino  
CC The bond is less labile than a disulphide bond. The stable cyclic  
CC HIV PND peptides (CPND's) may be used as analytical tools and as reagents  
CC in ELISA assays. They may also be conjugated to an immunogenic carrier (a  
CC protein and/or a polysaccharide; e.g. PpP or OMPc) to give a product  
CC useful for inducing mammalian anti-peptide, anti-HIV, or HIV-neutralizing  
CC immune responses and for formulating vaccines to prevent HIV disease,  
CC including AIDS and ARC, or for treating humans afflicted with HIV disease  
CC such as AIDS or ARC  
XX  
XX Sequence 10 AA:  
90

Query Match	43.7%;	Score 31;	DB 2;	Length 10;
Best Local Similarity	83.3%;	Pred.No. 1.5e+02;		

Query Match	43.7%	Score 31;	DB 2;	Length 10;
Best Local Similarity	83.3%	Pred. No. 1.5e+02;		
Matches	5;	Conservative	0;	Mismatches 1; Indels 0; Gaps 0

Query March	43.7%;	Score 31;	DB 2;	Length 10;
Best Local Similarity	83.3%;	Pred. No.	1.5e+02;	
Matches	5;	Conservative	0;	Mismatches 1;
				Indels 0;
				Gaps 0
Oy	5 KHYGPG 10			

Qy	5 KHYSFG 10
Db	1 KHISFG 6

Oy	5	KHYGPG	10
Db	2	KHYGPG	7

RESULT 24  
AAR31293  
ID AAR31293 standard; peptide; 10 AA

```
RESULT 25
AAR31308
XX      AAR31308 standard, peptide, 10 AA
XX
AC      AAR31308;
XX
```

Accession	Protein
AC	AAR31293;
XX	
DT	11-FEB-1993 (first entry)
XX	
DE	Cyclic HIV principal neutralizing determinant peptide.
XX	

XX Cyclic HIV principal neutralizing determinant peptide.  
DE  
XX Cyclic; conjugate; AIDS; ARC; vaccine.  
XX Human immunodeficiency virus; PND; cyclic; conjugate;  
KM immunogen; Elish; analysis; CPND30.  
XX

xx	Synthetic.
OS	
xx	
FH	Key
FT	Modified-site
FT	
FT	Modified-site
FT	
FT	Modified-site
FT	
FT	Modified-site
FT	
Lys(2)	"forms cyclic amide bond with epsilon- NH2 of Lys(2)"

[illegible]

EN BF4/1453-A.  
 XX 19-FEB-1992.  
 PD 19-FEB-1992.  
 XX 19-JUL-1991;  
 PF 91EP-00306582.  
 XX 19-JUL-1990;  
 PR 90US-00555112.  
 XX  
 XX  
 XX (MERIT) MERCK & CO INC.  
 XX  
 XX

XX 19-JUL-1991; 91EP-00306582.  
 PF 19-JUL-1990; 90US-00555112.  
 XX 19-JUL-1990; 90US-00555112.  
 XX (MERI ) MERCK & CO INC.  
 XX  
 PF Sugg EE, Dolan CA, Bednarek MA, Tolman RJ, Christense BG,  
 XX 1990-000011/40

PI Suggs EE, Dolan CA, Bednarek MA, Tolman RL, Christensen BG,  
XX  
XX WPI, 1992-058511/08.  
DR  
XX New cyclic HIV principal neutralising determinant peptide(s) - used as  
PT laboratory tools and as vaccines against HIV, AIDS, etc etc.  
XX  
XX Claim 4; Page 20; 25pp; English.  
XX

XX New cyclic HIV principal neutralising determinant peptide(s) - used as  
 PT laboratory tools and as vaccines against HIV, AIDS, etc.  
 XX  
 XX Claim 4; Page 22; 25pp; English.  
 PS  
 XX The peptide (cPND30) is a specifically claimed example of HIV principal  
 CC neutralising determinant peptides which are covered generically in Claim 1



CC ELISA assays. They may also be conjugated to an immunogenic carrier (a  
CC protein and/or a polysaccharide, e.g. PRP or OMC) to give a product  
CC useful for inducing mammalian anti-peptide, anti-HIV, or HIV-neutralizing  
CC immune responses and for formulating vaccines to prevent HIV disease,  
CC including AIDS and ARC, or for treating humans afflicted with HIV disease  
CC such as AIDS or ARC  
CC  
SQ Sequence 10 AA;  
Query Match 43.7%; Score 31; DB 2; Length 10;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 5 KHYGPG 10  
DB 2 KHIGPG 7  
RESULT 26  
AAR31297  
ID AAR31297 standard; peptide; 10 AA.  
XX  
AC AAR31297;  
XX  
DT 11-FEB-1993 (first entry)  
XX  
DE Cyclic HIV principal neutralizing determinant peptide.  
XX  
KW Human immunodeficiency virus; PND; cyclic; conjugate; AIDS; ARC; vaccine;  
KW immunogen; ELISA; analysis; CPND14.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1 /label= Nle  
FT /note= "Z-Nle"  
FT Modified-site 2 /note= "D-Lys; and forms cyclic lactam bond, via epsilon-  
FT NH2, with C-terminal COOH"  
FT Modified-site 10 /note= "forms cyclic amide bond with epsilon- NH2 of  
FT Lys(2)"  
XX  
EN EP471453-A.  
XX  
PD 19-FEB-1992.  
XX  
PF 19-JUL-1991; 91EP-00306582.  
XX  
PR 19-JUL-1990; 90US-00555112.  
XX  
PA (MERI ) MERCK & CO INC.  
XX  
PI Sugg EE, Dolan CA, Bednarek MA, Tolman RL, Christense BG;  
XX WPI, 1992-056511/08.  
XX  
DR WPI, 1992-056511/08.  
XX  
PT New cyclic HIV principal neutralising determinant peptide(s) - used as  
PT laboratory tools and as vaccines against HIV, AIDS, arc etc.  
XX  
PS Claim 4; Page 20; 25pp; English.  
XX  
CC The peptide (CPND14) is a specifically claimed example of HIV principal  
CC neutralizing determinant peptides which are covered generically in Claims  
CC 1-3 (AAR31291, AAR31292), the peptides being stably cyclised as a result  
CC of a lactam bridge between an NH2 on the N-terminal side of the loop  
CC amino acids and a COOH on the C-terminal side of the loop amino acids.  
CC The bond is less labile than a disulphide bond. The stable cyclic HIV PND  
CC peptides (CPND's) may be used as analytical tools and as reagents in  
CC ELISA assays. They may also be conjugated to an immunogenic carrier (a  
CC protein and/or a polysaccharide; e.g. PRP or OMC) to give a product  
CC useful for inducing mammalian anti-peptide, anti-HIV, or HIV-neutralizing

CC immune responses and for formulating vaccines to prevent HIV disease,  
CC including AIDS and ARC, or for treating humans afflicted with HIV disease  
CC such as AIDS or ARC  
CC  
SQ Sequence 10 AA;  
Query Match 43.7%; Score 31; DB 2; Length 10;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 5 KHYGPG 10  
DB 2 KHIGPG 7  
RESULT 27  
AAR31305  
ID AAR31305 standard; peptide; 10 AA.  
XX  
AC AAR31305;  
XX  
DT 11-FEB-1993 (first entry)  
XX  
DE Cyclic HIV principal neutralizing determinant peptide.  
XX  
KW Human immunodeficiency virus; PND; cyclic; conjugate; AIDS; ARC; vaccine;  
KW immunogen; ELISA; analysis; CPND27.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1 /label= Nle  
FT Modified-site 2 /note= "forms cyclic lactam bond, via epsilon-NH2, with C  
FT -terminal COOH"  
FT Modified-site 10 /note= "D-Phe; and forms cyclic amide bond with epsilon  
FT NH2 of Lys(2)"  
XX  
EN EP471453-A.  
XX  
PD 19-FEB-1992.  
XX  
PF 19-JUL-1991; 91EP-00306582.  
XX  
PR 19-JUL-1990; 90US-00555112.  
XX  
PA (MERI ) MERCK & CO INC.  
XX  
PI Sugg EE, Dolan CA, Bednarek MA, Tolman RL, Christense BG;  
XX WPI, 1992-056511/08.  
XX  
DR WPI, 1992-056511/08.  
XX  
PT New cyclic HIV principal neutralising determinant peptide(s) - used as  
PT laboratory tools and as vaccines against HIV, AIDS, arc etc.  
XX  
PS Claim 4; Page 22; 25pp; English.  
XX  
CC The peptide (CPND27) is a specifically claimed example of HIV principal  
CC neutralizing determinant peptides which are covered generically in Claims  
CC 1-3 (AAR31291, AAR31292), the peptides being stably cyclised as a result  
CC of a lactam bridge between an NH2 on the N-terminal side of the loop  
CC amino acids and a COOH on the C-terminal side of the loop amino acids.  
CC The bond is less labile than a disulphide bond. The stable cyclic HIV PND  
CC peptides (CPND's) may be used as analytical tools and as reagents in  
CC ELISA assays. They may also be conjugated to an immunogenic carrier (a  
CC protein and/or a polysaccharide; e.g. PRP or OMC) to give a product  
CC useful for inducing mammalian anti-peptide, anti-HIV, or HIV-neutralizing  
CC immune responses and for formulating vaccines to prevent HIV disease,  
CC including AIDS and ARC, or for treating humans afflicted with HIV disease  
CC such as AIDS or ARC

SQ Sequence 10 AA; 43.7%; Score 31; DB 2; Length 10;  
Query Match Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHYGPG 10  
|||  
2 KHIGPG 7

Db 2 KHIGPG 7

RESULT 28  
AAR26696  
ID AAR26696 standard; peptide; 10 AA.  
XX  
AC AAR26696;  
XX  
DT 09-FEB-1993 (first entry)  
XX  
DE HIV-PND-polysaccharide-protein conjugate vaccine.  
XX  
KM Human immunodeficiency virus; principal neutralizing determinant;  
outer membrane protein complex; OMPC; Neisseria; AIDS; cyclic; CPND14.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1 /label= Nle  
FT /note= "bonded via N-terminal to polysaccharide- protein  
FT complex"  
FT Modified-site 2 /note= "D-Lys; epsilon-amino forms cyclic peptide with C-  
FT terminal COOH group"  
FT Modified-site 10 /note= "condenses with side chain NH2 of Lys(2) to give  
FT cyclic peptide"  
XX  
PN EP468714-A.  
XX  
PD 29-JAN-1992.  
XX  
PF 19-JUL-1990; 90US-00555558.  
XX  
PR 19-JUL-1990; 90US-00555558.  
PR 19-JUL-1990; 90US-00555974.  
PR 19-JUN-1991; 91US-00715275.  
PR 19-JUN-1991; 91US-00715277.  
XX  
PA (MERI ) MERCK & CO INC.  
XX  
PI Marburg S, Tolman RL, Emini EA;  
XX  
DR WPI; 1992-034437/05.  
XX  
PT HIV peptide-polysaccharide-protein conjugates - used in vaccines or to  
XX produce antibodies to prevent or treat HIV infection.  
XX  
PS Claim 9; Page 54; 63pp; English.  
XX  
XX The invention relates to a conjugate of an HIV principal neutralizing  
determinant (PND), or an immunologically equivalent peptide (PEP),  
covalently coupled to an immunogenic protein or protein complex through  
an anionic polysaccharide linker. Pref. the immunogenic protein is the  
outer membrane protein complex (OMPC) of Neisseria meningitidis b and the  
PND peptide has a linear structure, a disulphide-bonded cyclic structure,  
an amide-bonded cyclic structure or a thioether-bonded cyclic structure.  
The present sequence (CPND14) is an example of a PND peptide component.  
The conjugates are used for inducing HIV-neutralizing antibodies or for  
making vaccines to prevent contraction of HIV infection or disease. The  
antibodies can be used for passively protecting against infection by HIV,  
or for protecting against proliferation of HIV post-infection, or for  
treating AIDS, or in diagnostic assays

XX SQ Sequence 10 AA; 43.7%; Score 31; DB 2; Length 10;  
Query Match Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHYGPG 10  
|||  
2 KHIGPG 7

Db 2 KHIGPG 7

RESULT 29  
AAR26691  
ID AAR26691 standard; peptide; 10 AA.  
XX  
AC AAR26691;  
XX  
DT 09-FEB-1993 (first entry)  
XX  
DE HIV-PND-polysaccharide-protein conjugate vaccine.  
XX  
KM Human immunodeficiency virus; principal neutralizing determinant;  
outer membrane protein complex; OMPC; Neisseria; AIDS; cyclic; CPND8.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1 /label= Nle  
FT /note= "bonded via N-terminal to polysaccharide- protein  
FT complex"  
FT Modified-site 2 /note= "epsilon-amino forms cyclic peptide with C-  
FT terminal COOH group"  
FT Modified-site 10 /note= "condenses with side chain NH2 of Lys(2) to give  
FT cyclic peptide"  
XX  
PN EP468714-A.  
XX  
PD 29-JAN-1992.  
XX  
PF 19-JUL-1990; 90US-00555558.  
XX  
PR 19-JUL-1990; 90US-00555558.  
PR 19-JUL-1990; 90US-00555974.  
PR 19-JUN-1991; 91US-00715275.  
PR 19-JUN-1991; 91US-00715277.  
XX  
PA (MERI ) MERCK & CO INC.  
XX  
PI Marburg S, Tolman RL, Emini EA;  
XX  
DR WPI; 1992-034437/05.  
XX  
PT HIV peptide-polysaccharide-protein conjugates - used in vaccines or to  
XX produce antibodies to prevent or treat HIV infection.  
XX  
PS Claim 9; Page 54; 63pp; English.  
XX  
XX The invention relates to a conjugate of an HIV principal neutralizing  
determinant (PND), or an immunologically equivalent peptide (PEP),  
covalently coupled to an immunogenic protein or protein complex through  
an anionic polysaccharide linker. Pref. the immunogenic protein is the  
outer membrane protein complex (OMPC) of Neisseria meningitidis b and the  
PND peptide has a linear structure, a disulphide-bonded cyclic structure,  
an amide-bonded cyclic structure or a thioether-bonded cyclic structure.  
The present sequence (CPND8) is an example of a PND peptide component.  
The conjugates are used for inducing HIV-neutralizing antibodies or for  
making vaccines to prevent contraction of HIV infection or disease. The  
antibodies can be used for passively protecting against infection by HIV,  
or for protecting against proliferation of HIV post-infection, or for

CC creating AIDS, or in diagnostic assays  
 XX  
 SQ Sequence 10 AA;  
 Query Match 43.7%; Score 31; DB 2; Length 10;  
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 5 KRYGPG 10  
 |||||  
 Db 2 KHIGPG 7  
 RESULT 30  
 AAR26707  
 ID AAR26707 standard; peptide; 10 AA.  
 XX  
 AC AAR26707;  
 XX  
 DT 09-FEB-1993 (first entry)  
 XX  
 DE HIV-PND-polysaccharide-protein conjugate vaccine.  
 XX  
 KW Human immunodeficiency virus; principal neutralizing determinant;  
 KW outer membrane protein complex; OMPC; Neisseria; AIDS; cyclic; CPND30.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1 /label= Nle  
 FT /note= "bonded via N-terminal to polysaccharide- protein complex"  
 FT Modified-site 2 /note= "epsilon-amino forms cyclic peptide with C-terminal COOH group"  
 FT Modified-site 10 /note= "condenses with side chain NH2 of Lys(2) to give cyclic peptide"  
 EP468714-A.  
 PD 29-JAN-1992.  
 XX  
 PF 19-JUL-1990; 90US-00555558.  
 XX  
 PR 19-JUL-1990; 90US-00555558.  
 PR 19-JUL-1990; 90US-00555974.  
 PR 19-JUN-1991; 91US-00715275.  
 PR 19-JUN-1991; 91US-00715277.  
 XX  
 PA (MERI ) MERCK & CO INC.  
 XX  
 PI Marburg S, Tolman RL, Emini EA;  
 XX  
 DR WPI; 1992-034437/05.  
 FT HIV peptide-polysaccharide-protein conjugates - used in vaccines or to produce antibodies to prevent or treat HIV infection.  
 XX  
 PS Claim 9; Page 56; 63pp; English.  
 XX  
 CC The invention relates to a conjugate of an HIV principal neutralizing determinant (PND), or an immunologically equivalent peptide (PEP), covalently coupled to an immunogenic protein or protein complex through an antionic polysaccharide linker. Pref. the immunogenic protein is the outer membrane protein complex (OMPC) of Neisseria meningitidis b and the PND peptide has a linear structure, a disulphide-bonded cyclic structure, an amide-bonded cyclic structure or a thioether-bonded cyclic structure. The present sequence (CPND30) is an example of a PND peptide component. The conjugates are used for inducing HIV-neutralizing antibodies or for making vaccines to prevent contraction of HIV infection or disease. The antibodies can be used for passively protecting against infection by HIV,

CC or for protecting against proliferation of HIV post-infection, or for creating AIDS, or in diagnostic assays  
 XX  
 SQ Sequence 10 AA;  
 Query Match 43.7%; Score 31; DB 2; Length 10;  
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 5 KRYGPG 10  
 |||||  
 Db 2 KHIGPG 7  
 RESULT 31  
 AAR26708  
 ID AAR26708 standard; peptide; 10 AA.  
 XX  
 AC AAR26708;  
 XX  
 DT 09-FEB-1993 (first entry)  
 XX  
 DE HIV-PND-polysaccharide-protein conjugate vaccine.  
 XX  
 KW Human immunodeficiency virus; principal neutralizing determinant;  
 KW outer membrane protein complex; OMPC; Neisseria; AIDS; cyclic; CPND31.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1 /note= "N(epsilon)-condensed by Nle, where the N-terminal of the Nle bonds to polysaccharide- protein complex; N(alpha)-condensed by omega-COOH of Glu(10) to give cyclic peptide"  
 FT Modified-site 10 /note= "Glu-NH2; where omega-COOH condenses onto alpha-NH2 of Lys(1) to form cyclic peptide"  
 EP468714-A.  
 PD 29-JAN-1992.  
 XX  
 PF 19-JUL-1990; 90US-00555558.  
 XX  
 PR 19-JUL-1990; 90US-00555558.  
 PR 19-JUL-1990; 90US-00555974.  
 PR 19-JUN-1991; 91US-00715275.  
 PR 19-JUN-1991; 91US-00715277.  
 XX  
 PA (MERI ) MERCK & CO INC.  
 XX  
 PI Marburg S, Tolman RL, Emini EA;  
 XX  
 DR WPI; 1992-034437/05.  
 FT HIV peptide-polysaccharide-protein conjugates - used in vaccines or to produce antibodies to prevent or treat HIV infection.  
 XX  
 PS Claim 9; Page 56; 63pp; English.  
 XX  
 CC The invention relates to a conjugate of an HIV principal neutralizing determinant (PND), or an immunologically equivalent peptide (PEP), covalently coupled to an immunogenic protein or protein complex through an antionic polysaccharide linker. Pref. the immunogenic protein is the outer membrane protein complex (OMPC) of Neisseria meningitidis b and the PND peptide has a linear structure, a disulphide-bonded cyclic structure, an amide-bonded cyclic structure or a thioether-bonded cyclic structure. The present sequence (CPND31) is an example of a PND peptide component. The conjugates are used for inducing HIV-neutralizing antibodies or for making vaccines to prevent contraction of HIV infection or disease. The antibodies can be used for passively protecting against infection by HIV, or for protecting against proliferation of HIV post-infection, or for

CC treating AIDS, or in diagnostic assays  
 XX  
 SQ Sequence 10 AA;

Query Match 43.7%; Score 31; DB 2; Length 10;  
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHYGPG 10  
 |||||  
 DB 1 KHIGPG 6

## RESULT 32

AA026704  
 ID AA026704 standard; peptide; 10 AA.

AC AA026704;

DT 09-FEB-1993 (first entry)

DE HIV-PND-polysaccharide-protein conjugate vaccine.

KM Human immunodeficiency virus; principal neutralizing determinant;  
 KW outer membrane protein complex; OMPC; Neisseria; AIDS; cyclic; CPND27.

OS Synthetic.

PH Key Location/Qualifiers

FT Modified-site 1

FT Modified-site 2

FT Modified-site 3

FT Modified-site 4

FT Modified-site 5

FT Modified-site 6

FT Modified-site 7

FT Modified-site 8

FT Modified-site 9

FT Modified-site 10

FT Modified-site 11

FT Modified-site 12

FT Modified-site 13

FT Modified-site 14

FT Modified-site 15

FT Modified-site 16

FT Modified-site 17

FT Modified-site 18

FT Modified-site 19

FT Modified-site 20

FT Modified-site 21

The invention relates to a conjugate of an HIV principal neutralizing determinant (PND), or an immunologically equivalent peptide (PEP), covalently coupled to an immunogenic protein or protein complex through an antitonic polysaccharide linker. Pref. the immunogenic protein is the outer membrane protein complex (OMPC) of *Neisseria meningitidis* b and the PND peptide has a linear structure, a disulphide-bonded cyclic structure, an amide-bonded cyclic structure or a thioether-bonded cyclic structure. The present sequence (CPND27) is an example of a PND peptide component. The conjugates are used for inducing HIV-neutralizing antibodies or for making vaccines to prevent contraction of HIV infection or disease. The antibodies can be used for passively protecting against infection by HIV,

CC or for protecting against proliferation of HIV post-infection, or for  
 CC treating AIDS, or in diagnostic assays  
 XX  
 SQ Sequence 10 AA;

Query Match 43.7%; Score 31; DB 2; Length 10;  
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHYGPG 10  
 |||||  
 DB 2 KHIGPG 7

## RESULT 33

AA03407  
 ID AA03407 standard; peptide; 10 AA.

AC AA03407;

DT 10-OCT-1996 (first entry)

DE HIV principal neutralizing determinant CPND8.

KM conjugate; PND; HIV; principal neutralizing determinant; OMPC;  
 KW outer membrane protein complex; antitonic spacer; vaccine;  
 KM human immunodeficiency virus; water-soluble.

OS Synthetic.

PH Key Location/Qualifiers

FT Modified-site 1

FT Modified-site 2

FT Modified-site 3

FT Modified-site 4

FT Modified-site 5

FT Modified-site 6

FT Modified-site 7

FT Modified-site 8

FT Modified-site 9

FT Modified-site 10

FT Modified-site 11

FT Modified-site 12

FT Modified-site 13

FT Modified-site 14

FT Modified-site 15

FT Modified-site 16

FT Modified-site 17

FT Modified-site 18

FT Modified-site 19

FT Modified-site 20

FT Modified-site 21

A new conjugate immunogen comprises (a) the OMPC of *Neisseria meningitidis* b as a protein carrier, (b) a principal neutralizing determinant (PND) of HIV as a peptide epitope against which immune responses are directed, and (c) a low mol. wt. antitonic spacer linking (a) and (b). The conjugate is water-soluble, yet can carry a high peptide epitope loading. It is useful as a vaccine against HIV. The present sequence is an example of a PND which can be used in the conjugate

SQ Sequence 10 AA;  
 Query Match 43.7%; Score 31; DB 2; Length 10;  
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHVGP 10  
 |||||  
 DB 2 KHVGP 7

RESULT 34  
 AAR31270  
 ID AAR31270 standard; peptide; 11 AA.  
 AC AAR31270;  
 DT 12-FEB-1993 (first entry)  
 DE HIV principal determinant peptide.  
 XX  
 XX AIDS; ARC; human immunodeficiency virus; vaccine; cyclic; Neisseria;  
 XX meningitidis b; outer membrane protein complex; OMPC; CPND29.  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH Modified-site 1  
 FT /label= Nle  
 FT /note= "this position is linked to the OMPC of the  
 FT conjugate"  
 FT 2  
 FT Modified-site  
 FT /note= "epsilon-amino group is condensed with C-terminal  
 FT COOH to form cyclic peptide"  
 FT 11  
 FT Modified-site  
 FT /note= "D-Val; and forms amide bond with epsilon-amino of  
 FT Lys(2) to give cyclic molecule"  
 FT 11  
 XX  
 XX EP467700-A.  
 XX  
 XX 22-JAN-1992.  
 XX  
 XX 19-JUL-1991; 91EP-00306598.  
 XX  
 XX 19-JUL-1990; 90US-00555339.  
 XX 19-JUL-1990; 90US-00555966.  
 XX 19-JUN-1991; 91US-00715276.  
 XX 19-JUN-1991; 91US-00715278.  
 XX  
 XX (MERI ) MERCK & CO INC.  
 XX  
 XX Leanza WJ, Marburg S, Tolman RL, Emini EA;  
 DR WPI; 1992-026505/04.  
 XX  
 XX Conjugate proteins comprising HIV peptide components - useful for  
 PT preparing vaccines for e.g. AIDS or for treating infections.  
 XX  
 XX Claim 12; Page 55; 63pp; English.

The invention relates to a co-conjugate comprising an immunogenic protein  
 or protein complex having a first set of covalent linkages to low  
 molecular weight moieties which have an anionic or polyanionic character  
 at physiological pH, and a second set of covalent linkages to peptides  
 comprising HIV principal neutralizing determinants (PND's) or  
 immunologically equivalent peptides. Preferably at least one set of the  
 covalent linkages is comprised of maleimide derivatives; the  
 (poly)anionic moiety is composed of one to five residues of the anionic  
 form of a carboxylic, sulphonic or phosphonic acid; the immunogenic  
 protein is the outer membrane protein complex (OMPC) of Neisseria  
 meningitidis b; and the PND peptide has a linear structure, a disulphide-  
 bonded cyclic structure, an amide-bonded cyclic structure or a thioether-  
 bonded cyclic structure. The present sequence (CPND29) is an example of a

CC PND peptide component used in the co-conjugate. The co-conjugate is  
 CC useful for inducing anti-peptide immune response in mammals, for inducing  
 CC HIV-neutralizing antibodies in mammals, for formulating vaccines to  
 CC prevent HIV infection or disease, including AIDS, or for treating humans  
 CC afflicted with HIV infection or disease

SQ Sequence 11 AA;  
 Query Match 43.7%; Score 31; DB 2; Length 11;  
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHVGP 10  
 |||||  
 DB 2 KHVGP 7

RESULT 35  
 AAR31257  
 ID AAR31257 standard; peptide; 11 AA.  
 AC AAR31257;  
 DT 12-FEB-1993 (first entry)  
 DE HIV principal determinant peptide.  
 XX  
 XX AIDS; ARC; human immunodeficiency virus; vaccine; cyclic; Neisseria;  
 XX meningitidis b; outer membrane protein complex; OMPC; CPND9.  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH Modified-site 1  
 FT /label= Ac-Cys  
 FT /note= "bonds via this site to the OMPC of the conjugate"  
 FT 2  
 FT Modified-site  
 FT /label= Nle  
 FT 3  
 FT Modified-site  
 FT /note= "epsilon-amino group is condensed with C-terminal  
 FT COOH to form cyclic peptide"  
 FT 11  
 FT Modified-site  
 FT /note= "Forms amide bond with epsilon-amino of Lys(3) to  
 FT give cyclic molecule"  
 FT 11  
 XX  
 XX EP467700-A.  
 XX  
 XX 22-JAN-1992.  
 XX  
 XX 19-JUL-1991; 91EP-00306598.  
 XX  
 XX 19-JUL-1990; 90US-00555339.  
 XX 19-JUL-1990; 90US-00555966.  
 XX 19-JUN-1991; 91US-00715276.  
 XX 19-JUN-1991; 91US-00715278.  
 XX  
 XX (MERI ) MERCK & CO INC.  
 XX  
 XX Leanza WJ, Marburg S, Tolman RL, Emini EA;  
 DR WPI; 1992-026505/04.  
 XX  
 XX Conjugate proteins comprising HIV peptide components - useful for  
 PT preparing vaccines for e.g. AIDS or for treating infections.  
 XX  
 XX Claim 12; Page 53; 63pp; English.

The invention relates to a co-conjugate comprising an immunogenic protein  
 or protein complex having a first set of covalent linkages to low  
 molecular weight moieties which have an anionic or polyanionic character  
 at physiological pH, and a second set of covalent linkages to peptides  
 comprising HIV principal neutralizing determinants (PND's) or  
 immunologically equivalent peptides. Preferably at least one set of the

CC covalent linkages is comprised of maleimide derivatives; the  
 CC (poly)anionic moiety is composed of one to five residues of the anionic  
 CC form of a carboxylic, sulphonic or phosphonic acid; the immunogenic  
 CC protein is the outer membrane protein complex (OMP) of *Neisseria*  
 CC meningitidis b; and the PND peptide has a linear structure, a disulphide-  
 CC bonded cyclic structure, an amide-bonded cyclic structure or a thioether-  
 CC bonded cyclic structure. The present sequence (CPND3) is an example of a  
 CC PND peptide component used in the co-conjugate. The co-conjugate is  
 CC useful for inducing anti-peptide immune response in mammals, for inducing  
 CC HIV-neutralizing antibodies in mammals, for formulating vaccines to  
 CC prevent HIV infection or disease, including AIDS, or for treating humans  
 CC afflicted with HIV infection or disease

CC Sequence 11 AA;

Query Match 43.7%; Score 31; DB 2; Length 11;  
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 KHGPG 10  
 |||||  
 3 KHGPG 8

RESULT 36

AAR31307  
 ID AAR31307 standard; peptide; 11 AA.

AC AAR31307;

DT 11-FEB-1993 (first entry)

DE Cyclic HIV principal neutralizing determinant peptide.

KM Human immunodeficiency virus; PND; cyclic; conjugate; AIDS; ARC; vaccine;  
 immunogen; ELISA; analysis; CPND3.

OS Synthetic.

Key Location/Qualifiers

FT Modified-site 1

FT /label= Nle

FT /note= "Z-Nle"

FT Modified-site 2

FT /note= "forms cyclic lactam bond, via epsilon-NH2, with C

FT -terminal COOH"

FT Modified-site 11

FT /note= "D-Val; and forms cyclic amide bond with epsilon

FT NH2 of Lys(2)"

FT XX

PN EP471453-A.

PD 19-FEB-1992.

PF 19-JUL-1991; 91EP-00306582.

PR 19-JUL-1990; 90US-00555112.

XX (MERI) MERCK & CO INC.

PA Sugg EE, Dolan CA, Bednarek MA, Tolman RL, Christense BG;

PI WPI; 1992-058511/08.

DR WPI; 1992-058511/08.

XX New cyclic HIV principal neutralizing determinant peptide(s) - used as

PT laboratory tools and as vaccines against HIV, AIDS, arc etc.

XX Claim 4; Page 22; 25pp; English.

XX The peptide (CPND3) is a specifically claimed example of HIV principal

CC neutralizing determinant peptides which are covered generically in Claims

CC 1-3 (AAR31291, AAR31292), the peptides being stably cyclised as a result

CC of a lactam bridge between an NH2 on the N-terminal side of the loop

CC amino acids and a COOH on the C-terminal side of the loop amino acids.

CC The bond is less labile than a disulphide bond. The stable cyclic HIV PND  
 CC peptides (CPND's) may be used as analytical tools and as reagents in  
 CC ELISA assays. They may also be conjugated to an immunogenic carrier (a  
 CC protein and/or a polysaccharide; e.g. PEP or OMP) to give a product  
 CC useful for inducing mammalian anti-peptide, anti-HIV, or HIV-neutralizing  
 CC immune responses and for formulating vaccines to prevent HIV disease,  
 CC including AIDS and ARC, or for treating humans afflicted with HIV disease  
 CC such as AIDS or ARC

CC Sequence 11 AA;

Query Match 43.7%; Score 31; DB 2; Length 11;  
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 KHGPG 10  
 |||||  
 2 KHGPG 7

RESULT 37

AAR31294  
 ID AAR31294 standard; peptide; 11 AA.

AC AAR31294;

DT 11-FEB-1993 (first entry)

DE Cyclic HIV principal neutralizing determinant peptide.

KM Human immunodeficiency virus; PND; cyclic; conjugate; AIDS; ARC; vaccine;  
 immunogen; ELISA; analysis; CPND3; CPND10.

OS Synthetic.

Key Location/Qualifiers

FT Modified-site 1

FT /note= "Ac-Cys (Acm) (giving CPND10) or Ac-Cys (giving

FT CPND3)"

FT Modified-site 2

FT /label= Nle

FT Modified-site 3

FT /note= "forms cyclic lactam bond, via epsilon-NH2, with C

FT -terminal COOH"

FT Modified-site 11

FT /note= "forms cyclic amide bond with epsilon- NH2 of

FT Lys(3)"

FT XX

PN EP471453-A.

PD 19-FEB-1992.

PF 19-JUL-1991; 91EP-00306582.

PR 19-JUL-1990; 90US-00555112.

XX (MERI) MERCK & CO INC.

PA Sugg EE, Dolan CA, Bednarek MA, Tolman RL, Christense BG;

PI WPI; 1992-058511/08.

DR WPI; 1992-058511/08.

XX New cyclic HIV principal neutralizing determinant peptide(s) - used as

PT laboratory tools and as vaccines against HIV, AIDS, arc etc.

XX Claim 4; Page 20; 25pp; English.

XX The peptides (CPND3 and CPND10) are specifically claimed examples of HIV

CC principal neutralizing determinant peptides which are covered generically

CC in Claims 1-3 (AAR31291, AAR31292), the peptides being stably cyclised as

CC a result of a lactam bridge between an NH2 on the N-terminal side of the

CC loop amino acids and a COOH on the C-terminal side of the loop amino

CC amino acids and a COOH on the C-terminal side of the loop amino

CC acids. The bond is less labile than a disulphide bond. The stable cyclic  
CC HIV PND peptides (CPND's) may be used as analytical tools and as reagents  
CC in ELISA assays. They may also be conjugated to an immunogenic carrier (a  
CC protein and/or a polysaccharide; e.g. PRP or OMP) to give a product  
CC useful for inducing mammalian anti-peptide, anti-HIV, or HIV-neutralizing  
CC immune responses and for formulating vaccines to prevent HIV disease,  
CC including AIDS and ARC, or for treating humans afflicted with HIV disease  
CC such as AIDS or ARC  
XX  
SQ Sequence 11 AA;

Query Match 43.7%; Score 31; DB 2; Length 11;  
Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHYGPG 10  
|||  
Db 3 KHIGPG 8

RESULT 38  
AAR26692

ID AAR26692 standard; peptide; 11 AA.

AC AAR26692;

DT 09-FEB-1993 (first entry)

XX HIV-PND-polysaccharide-protein conjugate vaccine.

XX Human immunodeficiency virus; principal neutralizing determinant;  
KW outer membrane protein complex; OMP; Neisseria; AIDS; cyclic; CPND9.

OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "Ac-Cys, bonded to polysaccharide- protein  
FT complex"

FT Modified-site 2 /label= Nle

FT Modified-site 3 /note= "epsilon-amino forms cyclic peptide with C-  
FT terminal COOH group"

FT Modified-site 11 /note= "condenses with side chain NH2 of Lys(3) to give  
FT cyclic peptide"

XX EP468714-A.

XX 29-JAN-1992.

XX 19-JUL-1990;

XX 90US-00555558.

XX 19-JUL-1990;

XX 90US-00555558.

XX 19-JUL-1990;

XX 90US-00555558.

XX 19-JUN-1991;

XX 91US-00715275.

XX 19-JUN-1991;

XX 91US-00715275.

XX (MERI ) MERCK & CO INC.

XX Marburg S, Tolman RL, Emimi EA;

XX WPI; 1992-034437/05.

CC an anionic polysaccharide linker. Pref. the immunogenic protein is the  
CC outer membrane protein complex (OMP) of Neisseria meningitidis b and the  
CC PND peptide has a linear structure, a disulphide-bonded cyclic structure,  
CC an amide-bonded cyclic structure or a thioether-bonded cyclic structure.  
CC The present sequence (CPND9) is an example of a PND peptide component.  
CC The conjugates are used for inducing HIV-neutralising antibodies or for  
CC making vaccines to prevent contraction of HIV infection or disease. The  
CC antibodies can be used for passively protecting against infection by HIV,  
CC or for protecting against proliferation of HIV post-infection, or for  
CC treating AIDS, or in diagnostic assays  
XX  
SQ Sequence 11 AA;

Query Match 43.7%; Score 31; DB 2; Length 11;  
Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHYGPG 10  
|||  
Db 3 KHIGPG 8

RESULT 39  
AAR26706

ID AAR26706 standard; peptide; 11 AA.

AC AAR26706;

DT 09-FEB-1993 (first entry)

XX HIV-PND-polysaccharide-protein conjugate vaccine.

XX Human immunodeficiency virus; principal neutralizing determinant;  
KW outer membrane protein complex; OMP; Neisseria; AIDS; cyclic; CPND2.

OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= Nle  
FT /note= "bonded via N-terminal to polysaccharide- protein  
FT complex"

FT Modified-site 2 /note= "epsilon-amino forms cyclic peptide with C-  
FT terminal COOH group"

FT Modified-site 11 /note= "D-Val; condenses with side chain NH2 of Lys(2) to  
FT give cyclic peptide"

XX EP468714-A.

XX 29-JAN-1992.

XX 19-JUL-1990;

XX 90US-00555558.

XX 19-JUL-1990;

XX 90US-00555558.

XX 19-JUL-1990;

XX 90US-00555558.

XX 19-JUN-1991;

XX 91US-00715275.

XX 19-JUN-1991;

XX 91US-00715275.

XX (MERI ) MERCK & CO INC.

XX Marburg S, Tolman RL, Emimi EA;

XX WPI; 1992-034437/05.

CC HIV peptide-polysaccharide-protein conjugates - used in vaccines or to  
CC produce antibodies to prevent or treat HIV infection.

CC Claim 9; Page 56; 63pp; English.

CC The invention relates to a conjugate of an HIV principal neutralizing  
CC determinant (PND), or an immunologically equivalent peptide (PEP),  
CC covalently coupled to an immunogenic protein or protein complex through

covalently coupled to an immunogenic protein or protein complex through an anionic polysaccharide linker. Pref. the immunogenic protein is the outer membrane protein complex (OMP) of *Neisseria meningitidis* b and the PND peptide has a linear structure, a thioether-bonded cyclic structure, an amide-bonded cyclic structure or a thioether-bonded cyclic structure. The present sequence (cPND29) is an example of a PND peptide component. The conjugates are used for inducing HIV-neutralizing antibodies or for making vaccines to prevent contraction of HIV infection or disease. The antibodies can be used for passively protecting against infection by HIV, or for protecting against proliferation of HIV post-infection, or for treating AIDS, or in diagnostic assays

XX Sequence 11 AA;

Query Match 43.7%; Score 31; DB 2; Length 11;  
Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHVGP 10  
DB 2 KHIGPG 7

RESULT 40

ABR95759 ID ABR95759 standard; peptide; 8 AA.

XX ABR95759;

DT 04-DEC-1996 (first entry)

DE Alpha-4Beta-1 integrin binding inhibitory peptide 56.

XX VCAM-1; vascular cell adhesion molecule-1; VLA-4; very late antigen-4;  
KW inhibitor; binding; white blood cell; migration; capillary wall;  
KW tissue damage; injury; fibronectin; extracellular matrix glycoprotein;  
KW CS1; CS5; H1; LDV; active site.

XX Synthetic.

OS Key Location/Qualifiers  
FH Modified-site 8  
FT /note="Pro-NH2"

XX US5510332-A.

XX 23-APR-1996.

XX 07-JUL-1994; 94US-00271830.

XX 07-JUL-1994; 94US-00271830.

XX (TEXA-) TEXAS BIOTECHNOLOGY CORP.

XX Beck PJ, Vanderslice P, Kogan TP, Ren K;

XX WPI; 1996-221274/22.

PT New peptide(s) based on the LDV domain of fibronectin - used for  
PT inhibiting binding of alpha-4, beta-1 integrin to VCAM-1, fibronectin or  
PT invasin.

XX Claim 4; Col 43-44; 35pp; English.

XX Vascular cell adhesion molecule-1 (VCAM-1) is protein found on the  
XX surface of endothelial cells that line the interior wall of capillaries.  
XX VCAM-1 recognizes and binds to the integrin alpha-4beta-1 (IA4B1; or VLA-  
XX 4 for very late antigen-4), a heterodimeric protein present on the  
XX surface of certain white blood cells. Binding of IA4B1 to VCAM-1 allows  
XX white blood cells to adhere to the capillary wall in areas where the  
XX tissue surrounding the capillary has been infected or damaged. Sometimes  
XX this white blood cell migration can become uncontrolled, with white blood  
XX cells flooding to the scene, causing widespread tissue damage. Cpts.

capable of blocking this process may be beneficial as therapeutic agents. IA4B1 also recognizes the extracellular matrix glycoprotein fibronectin. Three distinct IA4B1-binding sites have been identified within fibronectin. One site is found in the HepII region and is expressed in all isoforms; two others (CS1 and CS5) are present in the alternatively spliced type III connecting segments. CS1 has the higher affinity for IA4B1 and contains the tripeptide LDV as its minimal active site. CC Peptides ABR95704-805 are modeled after a portion of the CS1 peptide that include the LDV domain presented in such a way by its novel flanking CC sequence to produce a potent inhibitor of IA4B1 binding

XX Sequence 8 AA;

Query Match 42.3%; Score 30; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GPGW 11  
DB 1 GPGW 4

RESULT 41

ABP46859 ID ABP46859 standard; peptide; 8 AA.

XX ABP46859;

DT 19-AUG-2002 (first entry)

DE Human Blys binding scFv VH CDR3 SEQ ID 2870.

XX Blys, B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
KW common variable immunodeficiency; acquired immunodeficiency syndrome.

XX Homo sapiens.

XX WO200202641-A1.

XX 10-JAN-2002.

XX 15-JUN-2001; 2001WO-US019110.

XX 16-JUN-2000; 2000US-0212210P.

XX 17-OCT-2000; 2000US-0240816P.

XX 16-MAR-2001; 2001US-0276248P.

XX 21-MAR-2001; 2001US-0277379P.

XX 25-MAY-2001; 2001US-0293499P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX (CAMS-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX WPI; 2002-114759/15.

XX Claim 2; Page 3068; 3148pp; English.

XX This invention describes novel antibodies that immunospecifically bind to  
XX B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the  
XX tumour necrosis factor (TNF) super family and induces B cell  
XX proliferation and differentiation. The antibodies of the invention have  
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
XX antirheumatic and antiAIDS activity and can be used in vaccines to  
XX inhibit the expression and activity of Blys. The antibodies bind to Blys  
XX and so may be used to detect and quantitate the presence of Blys in



CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of Blys. They may also be  
 CC administered to treat diseases associated with aberrant Blys expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent  
 CC the antibodies and fragments of the antibodies described in the method of  
 CC the invention  
 CC  
 XX  
 SQ Sequence 8 AA;

Query Match 42.3%; Score 30; DB 5; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 GPGW 11  
 |||||  
 Db 2 GPGW 5

## RESULT 42

AA95363 ID AAP95363 standard; peptide; 9 AA.

AC AAP95363;

DT 30-MAR-1992 (first entry)

XX Variable region V3, found in the envelope protein gp120 of an AIDS or ARC  
 XX causing or related virus strain MAL.

XX Vaccine; AIDS; ARC; HIV; diagnosis.

OS AIDS virus.

XX EP311219-A.

XX 12-APR-1989.

XX 07-OCT-1988; 88EP-00202248.

XX 09-OCT-1987; 87NL-00002403.

XX (DIER-) STICHTING CENT DIER.

XX (UNAM) UNIT VAN AMSTERDAM.

XX (UYAM-) UNIT AMSTERDAM ZIEKENHUI.

XX Goudsmit J, Melen RH;

XX WPI; 1989-108193/15.

XX Oligopeptide(s) corresp. to beta-turn variable region of gp.120 - used  
 XX for diagnosis of and prodn of vaccines against AIDS and ARC.

XX Disclosure; Page 4; 7pp; English.

XX The peptides of the invention comprise the beta-turn AA SQ GPG or GPGR at  
 XX positions 312-314 or 312-315 in the AA numbering of HIV-111B (BH10) and  
 XX flanking AA SQs having a length equal to or greater than 1 and pref.

XX equal to or greater than 2 AAs; variants in which the GPG or GPGR SQ has  
 XX been replaced by a different beta-turn SQ; and variants in which the free  
 XX NH2-terminal gp AA and/or the free carboxyl terminal gp. AA has been  
 XX blocked or modified otherwise

XX Sequence 9 AA;

SQ

Query Match 42.3%; Score 30; DB 1; Length 9;  
 Best Local Similarity 80.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 HXPG 10  
 |::|||

Db 2 HFGPG 6

RESULT 43  
 AAR31288 ID AAR31288 standard; peptide; 9 AA.

XX AAR31288;

XX 12-FEB-1993 (first entry)

XX HIV principal determinant peptide.

XX AIDS; ARC; human immunodeficiency virus; vaccine; Neisseria;  
 XX meningitidis b; outer membrane protein complex; OMPC; PND-MAL.

XX Synthetic.

XX Key Location/Qualifiers

XX Modified-site 1 /note="bonds to the OMPC of the conjugate via this site"

XX EP467700-A.

XX 22-JAN-1992.

XX 19-JUL-1991; 91EP-00306598.

XX 19-JUL-1990; 90US-00555339.

XX 19-JUL-1990; 90US-00555366.

XX 19-JUN-1991; 91US-00715276.

XX 19-JUN-1991; 91US-00715278.

XX (MERI) MERCK & CO INC.

XX Leanza WJ, Marburg S, Tolman RL, Emimi EA;

XX WPI; 1992-026505/04.

XX Conjugate proteins comprising HIV peptide components - useful for  
 XX preparing vaccines for e.g. AIDS or for treating infections.

XX Claim 12; Page 56; 63pp; English.

XX The invention relates to a co-conjugate comprising an immunogenic protein  
 XX or protein complex having a first set of covalent linkages to low  
 XX molecular weight moieties which have an anionic or polyanionic character  
 XX at physiological pH, and a second set of covalent linkages to peptides  
 XX comprising HIV principal neutralizing determinants (PND's) or

XX immunologically equivalent peptides. Preferably at least one set of the  
 XX covalent linkages is comprised of maleimide derivatives; the  
 XX (poly)anionic moiety is composed of one to five residues of the anionic  
 XX form of a carboxylic, sulfonic or phosphonic acid; the immunogenic  
 XX protein is the outer membrane protein complex (OMPC) of Neisseria

XX meningitidis b; and the PND peptide has a linear structure, a disulphide-  
 XX bonded cyclic structure, an amide-bonded cyclic structure or a thioether-  
 XX bonded cyclic structure. The present sequence (PND-MAL) is an example of

XX a PND peptide component used in the co-conjugate. The co-conjugate is  
 XX useful for inducing anti-peptide immune response in mammals, for inducing  
 XX HIV-neutralizing antibodies in mammals, for formulating vaccines to  
 XX prevent HIV infection or disease, including AIDS, or for treating humans

XX afflicted with HIV infection or disease

XX Sequence 9 AA;

SQ

Query Match 42.3%; Score 30; DB 2; Length 9;  
 Best Local Similarity 80.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 HXPG 10  
 |::|||  
 Db 2 HFGPG 6



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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:34 ; Search time 10.5912 Seconds  
(without alignments)  
327.696 Million cell updates/sec

Title:	US-09-720-469A-6
Perfect score:	63
Sequence:	1 IYGERFPDENF 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

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Searched:      1017041 segs, 315518202 residues
Total number of hits satisfying chosen parameters: 3347
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Minimum DB seq length: 8
Maximum DB seq length: 14
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Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

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1:  sp.archaea:*
2:  sp.bacteria:*
3:  sp.fungi:*
4:  sp.human:*
5:  sp.invertebrate:*
6:  sp.mammal:*
7:  sp.mic:*
8:  sp.organelle:*
9:  sp.phage:*
10: sp.plant:*
11: sp.rodent:*
12: sp.virus:*
13: sp.yeast:*
14: sp_unclassified:*
15: sp_virus:*
16: sp.bacteriap:*
17: sp.archaeap:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	29	46.0	13	4	Q9UP27	Q9UP27 homo sapien
2	26	36.5	13	4	P96350	P96350 leionella
3	22	34.9	11	2	Q48933	Q48933 mycobacteri
4	22	34.9	14	11	Q93J75	Q93J75 mus musculu
5	20	31.7	10	2	P96352	P96352 marinobacte
6	20	31.7	10	2	Q93JL5	Q93JL5 photobacter
7	20	31.7	10	2	P96321	P96321 escherichia
8	20	31.7	10	2	P96306	P96306 aeromonas s
9	20	31.7	13	13	Q8J32	Q8J32 ficedula a
10	20	31.7	13	13	Q9PS56	Q9PS56 carassius a
11	20	31.7	14	4	Q75S0	Q75S0 homo sapien
12	19	30.2	13	4	Q8WY56	Q8WY56 homo sapien
13	18	28.6	10	2	Q8XHN9	Q8XHN9 clostridium
14	18	28.6	10	4	Q75A2	Q75A2 homo sapien
15	18	28.6	10	8	Q85V65	Q85V65 eucalyptus
16	18	28.6	10	11	Q9QV7	Q9QV7 rattus sp.

## ALIGNMENTS

17	18	28.6	10	11	Q63389
16	18	28.6	10	11	Q63971
19	18	28.6	11	2	Q87882
20	18	28.6	13	4	Q30NV6
21	18	28.6	14	2	Q52840
22	18	28.6	14	2	Q52636
23	17	27.0	8	2	Q7X139
24	17	27.0	8	13	Q90ZV5
25	17	27.0	9	11	Q62530
26	17	27.0	10	2	Q48469
27	17	27.0	10	2	Q96305
28	17	27.0	10	4	Q9UN90
29	17	27.0	10	16	P96423
30	17	27.0	12	2	Q8GMM8
31	17	27.0	13	11	Q9CUD6
32	16	25.4	8	10	Q8GTG5
33	16	25.4	11	2	Q47604
34	16	25.4	11	3	Q9HFN8
35	16	25.4	11	5	Q9VJ48
36	16	25.4	11	6	Q9TRM5
37	16	25.4	11	13	Q7T285
38	16	25.4	11	13	Q7T284
39	16	25.4	11	13	Q7T283
40	16	25.4	11	13	Q7SX72
41	16	25.4	11	13	Q7SX71
42	16	25.4	11	15	Q9D232
43	16	25.4	12	4	Q81VH0
44	16	25.4	12	10	Q9S8F0
45	16	25.4	12	12	Q88577
					Q63389 rattus norv
					Q967F1 mus sp., pro
					Q87882 mycobacteri
					Q9UN6 homo sapien
					Q52840 thizobium 1
					Q52636 escherichia
					Q7X139 staphylococ
					Q90ZV5 fulica leuc
					Q62530 mus spretus
					Q48469 klebsiella
					Q96305 alteromonas
					Q9UN90 homo sapien
					P96423 pseudomonas
					Q8GMM8 acinetobact
					Q9CUD6 mus musculu
					Q8GTG5 lycopersico
					Q47604 escherichia
					Q9HFN8 candida rug
					Q9VJ48 aedes aegypt
					Q9TRM5 bos taurus
					Q7T285 geochelone
					Q7T284 geochelone
					Q7T283 geochelone
					Q7SX72 geochelone
					Q7SX71 geochelone
					Q9D232 human immun
					Q81VH0 homo sapien
					Q9S8F0 zea mays (m
					Q88577 theller's e

QY 4 ERPPDENF 11  
 DB 1 ERPPSHRF 8

## RESULT 2

ID P96350 PRELIMINARY; PRT; 14 AA.  
 AC P96350;  
 DT 01-MAY-1997 (TEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TEMBLrel. 03, Last sequence update)  
 DT 01-NOV-1998 (TEMBLrel. 08, Last annotation update)  
 DE Coded portion of proteolysis tag (Fragment).  
 OS Legionella pneumophila.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;  
 OC Legionellaceae; Legionella.  
 GN NCB1\_TaxID=446;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 33152;  
 RX MEDLINE=97128184; PubMed=8972778;  
 RA Williams K.P., Bartel D.P.;  
 RT "Phylogenetic analysis of tmRNA secondary structure."  
 RL RNA 2:1306-1310(1996).  
 DR EMBL; U68079; AAB8026.1; -.  
 FT NON TER 1  
 SQ SEQUENCE 14 AA; 1349 MW; C55F7318D3BE7D7D CRC64;

Query Match Best Local Similarity 100.0%; Score 23; DB 2; Length 14;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 DENF 11  
 DB 3 DENF 6

RESULT 3  
 ID Q48933 PRELIMINARY; PRT; 11 AA.  
 AC Q48933; P77701; Q48932;  
 DT 01-NOV-1996 (TEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TEMBLrel. 08, Last annotation update)  
 DE Alkyl hydroperoxide reductase C (Fragment).  
 GN AHPC.  
 OS Mycobacterium bovis.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OX NCB1\_TaxID=1765;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC35728; and ATCC35727;  
 RA Zhang Y., Dereic V.;  
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC35735;  
 RX MEDLINE=96236622; PubMed=8655566;  
 RA Dhandayuthapani S., Zhang Y., Dereic V.;  
 RT "Oxidative stress response and its role in sensitivity to isoniazid in Mycobacterium smegmatis and lack of expression in M. aurum and M. tuberculosis";  
 RT J Bacteriol. 178:3641-3649(1996).  
 RL EMBL; U58031; AAB00320.1; -.  
 DR EMBL; U57979; AAB99830.1; -.  
 DR EMBL; U57978; AAB99829.1; -.  
 DR EMBL; U57762; AAB00317.1; -.  
 FT NON TER 11  
 SQ SEQUENCE 11 AA; 1231 MW; 455099E3A87041A7 CRC64;

Query Match 34.9%; Score 22; DB 2; Length 11;

Best Local Similarity 60.0%; Pred. No. 2.5e+03;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 GERFP 7  
 DB 7 GDQFP 11

## RESULT 4

ID Q9JUS PRELIMINARY; PRT; 14 AA.  
 AC Q9JUS;  
 DT 01-OCT-2000 (TEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)  
 DE B-Raf protein (Fragment).  
 GN B-Raf.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCB1\_TaxID=10090;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RA Barnier J.V.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 [2]  
 RP SEQUENCE FROM N.A.  
 RA Barnier J.V., Papin C., Eychene A., Lecog O.;  
 RT "The mouse B-raf gene encodes multiple protein isoforms with tissue-specific expression.";  
 RL U. Biochem. 270:23381-23389(1995).  
 DR EMBL; A0276308; CAB81556.1; -.  
 FT NON TER 1  
 SQ SEQUENCE 14 AA; 1748 MW; D1E0505C44927F02 CRC64;

Query Match Best Local Similarity 34.9%; Score 22; DB 11; Length 14;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 ERPPD 8  
 DB 2 ERPPE 6

RESULT 5  
 ID P96352 PRELIMINARY; PRT; 10 AA.  
 AC P96352;  
 DT 01-MAY-1997 (TEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TEMBLrel. 03, Last sequence update)  
 DT 01-MAR-2001 (TEMBLrel. 16, Last annotation update)  
 DE Coded portion of proteolysis tag (Fragment).  
 OS Marinobacter hydrocarbonoclasticus (Pseudomonas nautica).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;  
 OC Alteromonadaceae; Marinobacter.  
 OX NCB1\_TaxID=2743;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 49840;  
 RX MEDLINE=97128184; PubMed=8972778;  
 RA Williams K.P., Bartel D.P.;  
 RT "Phylogenetic analysis of tmRNA secondary structure."  
 RL RNA 2:1306-1310(1996).  
 DR EMBL; U68077; AAB8027.1; -.  
 FT NON TER 1  
 SQ SEQUENCE 10 AA; 1051 MW; 857BD22DCB544B1A CRC64;

Query Match Best Local Similarity 31.7%; Score 20; DB 2; Length 10;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 DENF 11

Db 3 DENY 6

## RESULT 6

ID 093LES PRELIMINARY; PRT; 10 AA.

AC 093LES; 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

OS Proteolysis tag (Fragment).

OC Photobacterium phosphoreum.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;

OC Vibrionaceae; Photobacterium.

OX NCBI\_TaxID=659;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=20063247; PubMed=10592213;

RA Williams K.P.;

RT "The tRNA website.";

RL Nucleic Acids Res. 28:168-168(2000).

RN [2]

RP SEQUENCE FROM N.A.

RA Williams K.P.;

RT "Phylogenetic analysis of tRNA.";

RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY040837; AAK83525.1; -.

FT NON\_TER 1

SQ SEQUENCE 10 AA; 1051 MW; 857BD22DCB544B1A CRC64;

Query Match 31.7%; Score 20; DB 2; Length 10;

Best Local Similarity 75.0%; Pred. No. 5.3e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 DENF 11

Db 3 DENY 6

Query Match 31.7%; Score 20; DB 2; Length 10;

Best Local Similarity 75.0%; Pred. No. 5.3e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 DENF 11

Db 3 DENY 6

Query Match 31.7%; Score 20; DB 2; Length 10;

Best Local Similarity 75.0%; Pred. No. 5.3e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 DENF 11

Db 3 DENY 6

Query Match 31.7%; Score 20; DB 2; Length 10;

Best Local Similarity 75.0%; Pred. No. 5.3e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 DENF 11

Db 3 DENY 6

Query Match 31.7%; Score 20; DB 2; Length 10;

Best Local Similarity 75.0%; Pred. No. 5.3e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 DENF 11

Db 3 DENY 6

Query Match 31.7%; Score 20; DB 2; Length 10;

Best Local Similarity 75.0%; Pred. No. 5.3e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 DENF 11

Db 3 DENY 6

Query Match 31.7%; Score 20; DB 2; Length 10;

Best Local Similarity 75.0%; Pred. No. 5.3e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 DENF 11

Db 3 DENY 6

Query Match 31.7%; Score 20; DB 2; Length 10;

Best Local Similarity 75.0%; Pred. No. 5.3e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 DENF 11

Db 3 DENY 6

Query Match 31.7%; Score 20; DB 2; Length 10;

Best Local Similarity 75.0%; Pred. No. 5.3e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 DENF 11

Db 3 DENY 6

Query Match 31.7%; Score 20; DB 2; Length 10;

Best Local Similarity 75.0%; Pred. No. 5.3e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 DENF 11

Db 3 DENY 6

Query Match 31.7%; Score 20; DB 2; Length 10;

Best Local Similarity 75.0%; Pred. No. 5.3e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 DENF 11

Db 3 DENY 6

Query Match 31.7%; Score 20; DB 2; Length 10;

Best Local Similarity 75.0%; Pred. No. 5.3e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 DENF 11

Db 3 DENY 6

Query Match 31.7%; Score 20; DB 2; Length 10;

Best Local Similarity 75.0%; Pred. No. 5.3e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 DENF 11

Db 3 DENY 6

Query Match 31.7%; Score 20; DB 2; Length 10;

Best Local Similarity 75.0%; Pred. No. 5.3e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 DENF 11

Db 3 DENY 6

Query Match 31.7%; Score 20; DB 2; Length 10;

Best Local Similarity 75.0%; Pred. No. 5.3e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 DENF 11

Db 3 DENY 6

Query Match 31.7%; Score 20; DB 2; Length 10;

Best Local Similarity 75.0%; Pred. No. 5.3e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 DENF 11

Db 3 DENY 6

Query Match 31.7%; Score 20; DB 2; Length 10;

Best Local Similarity 75.0%; Pred. No. 5.3e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 DENF 11

Db 3 DENY 6

Query Match 31.7%; Score 20; DB 2; Length 10;

Best Local Similarity 75.0%; Pred. No. 5.3e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 DENF 11

Db 3 DENY 6

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RESULT 10
QPS56 PRELIMINARY; PRT; 13 AA.
AC QPS56;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE NEUROLIN=CELL surface glycoprotein (Fragment).
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN (1)
RP SEQUENCE.
RX MEDLINE=92250720; PubMed=1577862;
RA Paschke K.A., Lotzspeich F., Stuenkel C.A.;
RT "Nemolyn, a cell surface glycoprotein on growing retinal axons in the
RT goldfish visual system, is reexpressed during retinal axonal
RT regeneration.";
RL J. Cell Biol. 117:863-875(1992).
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1332 MW; 33AF8F8C535728 CRC64;

Query Match
Best Local Similarity 31.7%; Score 20; DB 13; Length 13;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IYGE 4
DB 7 LYGE 10

RESULT 11
QZ550 PRELIMINARY; PRT; 14 AA.
AC QZ550;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RX TISSUE=Uterus;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,
RA Diachenko L., Narasimha K., Farmer A.A., Rubin G.M., Hong L.,
RA Stegleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uscin T.B., Toshiyuki S., Carninci P., Pirange C.,
RA Raha S.S., Locuelli N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Maman A.C., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buttefield Y.S.,
RA Krywinski M.I., Skalska U., Smallus D.E., Schercher A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).
RN (2)
RP SEQUENCE FROM N.A.

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RC TISSUE=Uterus;
RA Strausberg R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC054509; AAH54509.1; -
KM Hypothetical protein.
SQ SEQUENCE 14 AA; 1893 MW; 5A6D6F30B6465257 CRC64;

Query Match
Best Local Similarity 31.7%; Score 20; DB 4; Length 14;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IYGER 5
DB 7 LYGER 11

RESULT 12
Q8W56 PRELIMINARY; PRT; 13 AA.
AC Q8W56;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Epithelial sodium channel beta-3 subunit (Fragment).
GN SCN1B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RA Thomas C.P., Loftus R.W., Liu K.Z., Itani O.A.;
RT "Genomic organization of the 5' end of human beta ENaC and preliminary
RT characterization of its promoter.";
RL Am. J. Physiol. Renal Physiol. 0:0-0(2002).
DR EMBL; AF260228; AAL46197.1; -
DR GO; GO:0005216; Pilon channel activity; IEA.
KM Ionic channel.
FT NON_TER 13
FT NON_TER 13
SQ SEQUENCE 13 AA; 1437 MW; 1716D00275917724 CRC64;

Query Match
Best Local Similarity 30.2%; Score 19; DB 4; Length 13;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 DENF 11
DB 9 DXNF 12

RESULT 13
Q8KN9 PRELIMINARY; PRT; 10 AA.
AC Q8KN9;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DE 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE BONT/A (Fragment).
GN BONT/A.
OS Clostridium botulinum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1491;
RN (1)
RP SEQUENCE FROM N.A.
RA STRAIN=62A, and NCTC 2916;
RA Dineen S.S., Bradshaw M., Johnson E.A.;
RT "Comparison of the neurotoxin gene clusters in Clostridium botulinum
RT type A strains.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF461539; AAM75954.1; -
DR EMBL; AF461541; AAM75962.1; -
FT NON_TER 1
FT NON_TER 1

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SEQ SEQUENCE 10 AA; 1143 MW; 8721FA0B1863787A CRC64;

Query Match 28.6%; Score 18; DB 2; Length 10;  
Best Local Similarity 75.0%; Pred. No. 1.2e+04;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 YGER 5  
DB 5 WGER 8

RESULT 14

Q725A2 PRELIMINARY; PRT; 10 AA.

AC Q725A2; 01-OCT-2003 (TREMBlrel. 25, Created)

DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)

DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

OS Hypothetical protein.

OC Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OC NCBI\_TaxID=9606;

RP SEQUENCE FROM N.A.

RC TISSUE=Testis;

RA Fraai P., Fors-Petter S., Berger J.;

RT "A novel relative of Bubblegum."

RL Submitted (JUL-2003) to the EMBL/Genbank/DBJ databases.

DR EMBL; AJ577571; CAB2153.1; -

KM Hypothetical protein.

SEQ SEQUENCE 10 AA; 1086 MW; 622094D8786769D4 CRC64;

Query Match 28.6%; Score 18; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 RFP 7  
DB 3 RFP 5

RESULT 15

Q85V65 PRELIMINARY; PRT; 10 AA.

AC Q85V65; 01-JUN-2003 (TREMBlrel. 24, Created)

DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)

DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

OS Ribosomal protein L2 (Fragment).

OC Eucalyptus grandis (flooded gun).

OC Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC Myrtales; Myrtaceae; Eucalyptus.

OC NCBI\_TaxID=71139;

RP SEQUENCE FROM N.A.

RA Jones M.E., Shepherd M., Henry R.J., Delves A., Scher L.;

RT "Intraspecific chloroplast DNA variation and population structure in

RT Eucalyptus grandis revealed by single-strand conformation polymorphism

RT (SSCP)."

RL Submitted (APR-2002) to the EMBL/Genbank/DBJ databases.

DR EMBL; AF502121; AAP30826.1; -

DR GO; GO:0009507; Chloroplast; IEA.

DR CO; GO:0003735; Structural constituent of ribosome; IEA.

KW Chloroplast; Ribosomal protein.

FT NON\_TER

SEQ SEQUENCE 10 AA; 1205 MW; 5387F0140879C057 CRC64;

Query Match 28.6%; Score 18; DB 8; Length 10;  
Best Local Similarity 60.0%; Pred. No. 1.2e+04;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 YGER 5  
DB 4 IFGR 8

RESULT 16

Q9QVF7 PRELIMINARY; PRT; 10 AA.

AC Q9QVF7; 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

OS Beta 2-glycoprotein I, beta 2-GPI (Fragment).

OC Rattus sp.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OC NCBI\_TaxID=10118;

RP SEQUENCE

RX MEDLINE=92135065; PubMed=1777418;

RA Matsura E., Igarashi M., Igarashi Y., Nagae H., Ichikawa K.;

RT "Molecular definition of human beta 2-glycoprotein I (beta 2-GPI) by

RT alternation of anticardiolipin binding."

RL Int. Immunol. 3:1217-1221(1991).

FT NON\_TER

SEQ SEQUENCE 10 AA; 1100 MW; 94E681B767376E41 CRC64;

Query Match 28.6%; Score 18; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 PDE 9  
DB 7 PDE 9

RESULT 17

Q63389 PRELIMINARY; PRT; 10 AA.

AC Q63389; 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

OS Ornithine decarboxylase (ODC).

OC Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OC NCBI\_TaxID=10116;

RP SEQUENCE FROM N.A.

RA STRAIN=Sprague-Dawley; TISSUE=Testis;

RX MEDLINE=89255378; PubMed=2722815;

RA Wen L., Huang J.K., Blackshear P.J.;

RT "Rat ornithine decarboxylase gene. Nucleotide sequence, potential

RT regulatory elements, and comparison to the mouse gene."

RL J. Biol. Chem. 264:9016-9021(1989).

DR EMBL; J04791; AAA66163.1; -

DR PIR; B33710; B33710.

SEQ SEQUENCE 10 AA; 1074 MW; 30F6EB69D415BDC7 CRC64;

Query Match 28.6%; Score 18; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 RFP 7  
DB 6 RFP 8

RESULT 18  
Q90VF1 PRELIMINARY; PRT; 10 AA.  
AC Q90VF1  
DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)  
DE Protamine MP2 (Fragment).  
OS Mus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10095;  
RN [1]  
RP SEQUENCE.  
RA MEDLINE=92174934; PubMed=1541289;  
RA Chauviere M., Martingue A., Debatte M., Sautiere P., Chevallier P.;  
RT "Molecular characterization of six intermediate proteins in the  
RT processing of mouse protamine P2 precursor.";  
RL Eur. J. Biochem. 204:759-765(1992).  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 10 AA; 1280 MW; 01DD2975A06841B CRC64;  
Query Match 28.6%; Score 18; DB 11; Length 10;  
Best Local Similarity 50.0%; Pred. No. 1.2e+04;  
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 2 YGERPDE 9  
DB 3 YMRSPSE 10  
RESULT 19  
087882 PRELIMINARY; PRT; 11 AA.  
AC 087882;  
DT 01-NOV-1998 (TRENBLrel. 08, Created)  
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)  
DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)  
DE Alkyl hydroperoxide reductase (Fragment).  
GN Ahpc.  
OS Mycobacterium xenopi.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.  
OX NCBI\_TaxID=1789;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC19250;  
RX MEDLINE=98406038; PubMed=9733688;  
RA Pagan-Ramos E., Song J., McFalone M., Mudd M.H., Deretic V.;  
RT "Oxidative stress response and characterization of the oxyR-ahpc and  
RT furA-katG loci in Mycobacterium marinum.";  
RL J. Bacteriol. 180:4856-4864(1998).  
DR EMBL, U43810; AAC61663.1; -.  
FT NON\_TER 11  
FT NON\_TER 11  
SQ SEQUENCE 11 AA; 1147 MW; 45458CE1787041A7 CRC64;  
Query Match 28.6%; Score 18; DB 2; Length 11;  
Best Local Similarity 60.0%; Pred. No. 1.4e+04;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 3 GERPP 7  
DB 7 GGQFP 11  
RESULT 20  
Q9UNV6 PRELIMINARY; PRT; 13 AA.  
AC Q9UNV6;  
DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
DE Inosine monophosphatase 2 (Fragment).  
GN IMPA2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97463449; PubMed=9322233;  
RA Yoshikawa T., Turner G., Esterling L.E., Sanders A.R.,  
RA Detera-Madleigh S.D.;  
RT "A novel human myo-inositol monophosphatase gene, IMP.18p, maps to a  
RT susceptibility region for bipolar disorder.";  
RL Mol. Psychiatry 2:393-397(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92084187;  
RA Yoshikawa T., Padigaru M., Karkera J.D., Sharma M., Berrettini W.H.,  
RA Esterling L.E., Detera-Madleigh S.D.;  
RT "Genomic structure and novel variants of myo-inositol monophosphatase  
RT 2.";  
RL Mol. Psychiatry 5:165-171(2000).  
DR EMBL, AF085628; AAD22141.1; -.  
DR EMBL, AF085627; AAD22141.1; JOINED.  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 13 AA; 1491 MW; B8154075786DD401 CRC64;  
Query Match 28.6%; Score 18; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.6e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 RFP 7  
DB 7 RFP 9  
RESULT 21  
052840 PRELIMINARY; PRT; 14 AA.  
AC 052840;  
DT 01-NOV-1996 (TRENBLrel. 01, Created)  
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)  
DE Homology with C-terminus of other Rhizobium nodB genes.  
OS Rhizobium loti (Mesorhizobium loti).  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Phyllobacteriaceae; Mesorhizobium.  
OX NCBI\_TaxID=381;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97002748; PubMed=8850088;  
RA Scott D.B., Young C.A., Collins-Emerison J.M., Terragni E.A.,  
RA Rockman E.S., Lewis P.E., Pankhurst C.E.;  
RT "Novel and complex chromosomal arrangement of Rhizobium loti  
RT nodulation genes.";  
RL Mol. Plant Microbe Interact. 9:187-197(1996).  
DR EMBL, L06241; AAB47352.1; -.  
SQ SEQUENCE 14 AA; 1600 MW; 90C26EC32C8B34C5 CRC64;  
Query Match 28.6%; Score 18; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.8e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 RFP 7  
DB 9 RFP 11  
RESULT 22  
052636 PRELIMINARY; PRT; 14 AA.  
ID 052636



AC Q52636;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DS Tral protein (Fragment).  
GN Tral.  
OS Escherichia coli.  
OC Plasmid R124.  
CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
CC Enterobacteriaceae; Escherichia.  
CX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86059219; PubMed=2999074;  
RA Frost L.S., Finlay B.B., Ogenorth A., Paranchych W., Lee J.S.;  
RT "Characterization and sequence analysis of pilin from F-like  
RT plasmids". 164:1238-1247(1985).  
RL J. Bacteriol. 164:1238-1247(1985).  
DR EMBL; X03092; AAA92759.1; -;  
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.  
KW Plasmid.  
FT NON TER  
SQ SEQUENCE 14 AA; 1713 MW; 5CCA9118EB30E23 CRC64;

Query Match 28.6%; Score 18; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.8e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RFP 7  
DB 12 RFP 14

RESULT 23  
ID Q7X139 PRELIMINARY; PRT; 8 AA.  
AC Q7X139;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE SecE (Fragment).  
OC Staphylococcus cohnii.  
CC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
CX NCBI\_TaxID=29382;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=GFU9122;  
RA Morikawa K., Inose Y., Ohta T.;  
RT "A new Staphylococcal sigma factor in the conserved gene cassette:  
RT Functional significance and implication for the evolutionary  
RT processes". 199:1-10(2003).  
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY34840; AAO62607.1; -;  
FT NON TER  
SQ SEQUENCE 8 AA; 1014 MW; F0C9C44B1333DD6 CRC64;

Query Match 27.0%; Score 17; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ENF 11  
DB 5 ENF 7

RESULT 24  
ID Q90ZV5 PRELIMINARY; PRT; 8 AA.  
AC Q90ZV5;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Adenylate kinase (Fragment).

OS Pulica leucoptera.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Gruiformes; Rallidae; Pulica.  
CX NCBI\_TaxID=156758;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Shapiro L.H., Dumbacher J.P.;  
RT "Adenylate kinase intron 5: a new nuclear locus for avian  
RT systematics".  
RL Auk 118:248-255(2001).  
DR EMBL; AF307898; AAK43537.1; -;  
DR GO; GO:0016301; F:kinase activity; IEA.  
KW Kinase.  
FT NON TER  
SQ SEQUENCE 8 AA; 994 MW; 96333B19CB1B1866 CRC64;

Query Match 27.0%; Score 17; DB 13; Length 8;  
Best Local Similarity 75.0%; Pred. No. 1e+06;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GEF 6  
DB 2 GEF 5

RESULT 25  
ID Q62530 PRELIMINARY; PRT; 9 AA.  
AC Q62530;  
DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Osteocalcin (Gamma-carboxyglutamic acid-containing protein) (Bone  
DE GLA-protein) (BGP) (Fragment).  
GN BGLAP.  
OS Mus spretus (Western wild mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
CX NCBI\_TaxID=10096;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SPRET/EL;  
RX MEDLINE=94319082; PubMed=8043949;  
RA Ko M.S., Wang X., Horron J.H., Hagen M.D., Takahashi N., Maezaki Y.,  
RA Nadeau J.H.;  
RT "Genetic mapping of 40 cDNA clones on the mouse genome by PCR";  
RL Mamm. Genome 5:349-355(1994).  
CC -1- FUNCTION: THIS BONE PROTEIN, CONSTITUTES 1-2% OF THE TOTAL PROTEIN  
CC OF BONE. IT BINDS STRONGLY TO APATITE AND CALCIUM.  
CC -1- TISSUE SPECIFICITY: BONE.  
CC -1- PTM: GAMMA-CARBOXYGLUTAMIC ACID RESIDUES ARE FORMED BY VITAMIN K  
CC DEPENDENT CARBOXYLATION. THESE RESIDUES ARE ESSENTIAL FOR THE  
CC BINDING OF CALCIUM.  
DR EMBL; U05695; AAB60465.1; -;  
DR PIR; I49406; I49406.  
DR MGD; MGI:88156; Bglap1.  
FT NON TER  
SQ SEQUENCE 9 AA; 1135 MW; 5937E0586B504403 CRC64;

Query Match 27.0%; Score 17; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IYG 3  
DB 4 IYG 6

RESULT 26  
ID Q48469 PRELIMINARY; PRT; 10 AA.  
AC Q48469;

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DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Nitrogenase (Fragment)
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=573;

RN
  [1]
  SEQUENCE FROM N.A.
  RA MEDLINE=83346546; PubMed=6306580;
  RA Shen S.C., Xue Z.T., Kong Q.T., Wu Q.L.;
  RT "An open reading frame upstream from the nifH gene of Klebsiella
  RT pneumoniae."
  RL Nucleic Acids Res. 11:4241-4250(1983).
  DR EMBL; X01006; CAA25501.1; -.
  FT NON_TER
  SQ SEQUENCE 10 AA; 1173 MW; B13069SDDEA6C406 CRC64;

Query Match
Best Local Similarity 27.0%; Score 17; DB 2; Length 10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IYG 3
DB 8 IYG 10

RESULT 27
P66305 PRELIMINARY; PRT; 10 AA.
AC P66305;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Coded portion of proteolysis tag (Fragment)
DE Alteromonas haloplanktis (Pseudalteromonas haloplanktis).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Alteromonadaceae; Pseudalteromonas.
OX NCBI_TaxID=228;

RN
  [1]
  SEQUENCE FROM N.A.
  RA STRAIN=ATCC 14393;
  RC MEDLINE=97128184; PubMed=8972778;
  RA Williams K.P., Bartel D.P.;
  RT "Phylogenetic analysis of tmRNA secondary structure."
  RL RNA 2:1306-1310(1996).
  DR EMBL; U68076; AAB48021.1; -.
  FT NON_TER
  SQ SEQUENCE 10 AA; 1053 MW; 857BD235AB544AAA CRC64;

Query Match
Best Local Similarity 27.0%; Score 17; DB 2; Length 10;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 DENF 11
DB 3 DDNY 6

RESULT 28
Q9UN90 PRELIMINARY; PRT; 10 AA.
AC Q9UN90;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE Canalicular multispecific organic anion transporter (Fragment).
OS CMOAT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;

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RN
  [1]
  SEQUENCE FROM N.A.
  RA Tanaka T., Uchiyama T., Hinoshita E., Inokuchi A., Toh S., Wada M.,
  RA Nomoto M., Kohno K., Kuwano M.;
  RT "Sequence analysis and functional characterization of the 5'-flanking
  RT region of the human canalicular multispecific organic anion
  RT transporter/multidrug resistance protein 2 (CMOAT/WRP2) gene."
  RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
  DR EMBL; AF144630; AAD47599.1; -.
  FT NON_TER
  SQ SEQUENCE 10 AA; 1219 MW; 76F28CB44EB9C33B CRC64;

Query Match
Best Local Similarity 27.0%; Score 17; DB 4; Length 10;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 ERPPDENF 11
DB 3 ERFKNSTF 10

RESULT 29
P66423 PRELIMINARY; PRT; 10 AA.
AC P66423;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Coded portion of proteolysis tag (Translated portion of tmRNA gene
DE serA) (Fragment).
GN PA0826.1.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;

RN
  [1]
  SEQUENCE FROM N.A.
  RA STRAIN=ATCC 25330;
  RC MEDLINE=97128184; PubMed=8972778;
  RA Williams K.P., Bartel D.P.;
  RT "Phylogenetic analysis of tmRNA secondary structure."
  RL RNA 2:1306-1310(1996).
  RN [2]
  RP SEQUENCE FROM N.A.
  RC STRAIN=ATCC 15692 / PA01;
  RC MEDLINE=20437337; PubMed=10984043;
  RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
  RA Hickey M.J., Brinkman P.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
  RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
  RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
  RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
  RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
  RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
  RT opportunistic pathogen."
  RL Nature 406:959-964(2000).
  DR EMBL; U68078; AAB48029.1; -.
  DR EMBL; AE004517; AAO42616.1; -.
  KW Complete proteome.
  FT NON_TER
  SQ SEQUENCE 10 AA; 1037 MW; 857BD22DCB544AAA CRC64;

Query Match
Best Local Similarity 27.0%; Score 17; DB 16; Length 10;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 DENF 11
DB 3 DDNY 6

RESULT 30
Q8GMW8 PRELIMINARY; PRT; 12 AA.
ID Q8GMW8

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AC Q8GMN8;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Transposase (Fragment).
GN TNP106.
OS Acinetobacter sp. BM3.
OC Plasmid pKJH207.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
CX NCBI_TaxID=106395;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BM3; PLASMID=pKJH207;
RA Khodoli G.V., Yurleva O.V., Mindlin S.Z., Gorlenko Z.M.,
RA Nikiforov V.G.;
RT "pKJH2-like aberrant transposons and possible mechanisms of their
RT dissemination.";
RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BM3; PLASMID=pKJH207;
RA Khodoli G.V., Mindlin S.Z., Gorlenko Z.M., Yurleva O.V.,
RA Petrova M.A., Nikiforov V.G.;
RT "A young family of transposable adaptive DNA segments identified in
RT the Acinetobacter genus.";
RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ250234; CAC80781.1; -
DR EMBL; AJ468856; CAD31077.1; -
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Plasmid.
FT NON TER
SQ SEQUENCE 12 AA; 1457 MW; B5832A70F8F40871 CRC64;

Query Match
Best Local Similarity 27.0%; Score 17; DB 2; Length 12;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 YGERPDE 9
DB 5 HGRHFOGE 12

RESULT 31
Q9CTU6 PRELIMINARY; PRT; 13 AA.
AC Q9CTU6;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Zona pellucida binding protein (Fragment).
GN ZBP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
CX NCBI_TaxID=10090;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai Y., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Marsuda H.A., Ashburner M., Batilov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
RA Kuwari P., Lewis S., Matsuo Y., Nikaido I., Pescio G., Quackenbush J.,
RA Schiml L.W., Stabili F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Grewenstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gusninch S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

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RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kontsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK018876; BAB31470.1; -
DR MED; MG11855701; Zbp.
FT NON TER
SQ SEQUENCE 13 AA; 1404 MW; D6A4220999576B42 CRC64;

Query Match
Best Local Similarity 27.0%; Score 17; DB 11; Length 13;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGER 5
DB 6 YGAK 10

RESULT 32
Q8GTG5 PRELIMINARY; PRT; 8 AA.
AC Q8GTG5;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE WRKY transcription factor Iid-1 splice variant 2 (Fragment).
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Solanum.
CX NCBI_TaxID=4081;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Money Maker; TISSUE=Leaf;
RA Cagna G., Boes A., Ulker B., Zhou A., Manke D., Somasich I.E.;
RT "Comparison of WRKY group II transcription factors from plants.";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY157059; AAN71729.1; -
FT NON TER
SQ SEQUENCE 8 AA; 917 MW; 59177B47758B7330 CRC64;

Query Match
Best Local Similarity 25.4%; Score 16; DB 10; Length 8;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGERFP 7
DB 1 IKGSPY 7

RESULT 33
Q47604 PRELIMINARY; PRT; 11 AA.
AC Q47604;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Rease protein (Fragment).
GN REASE.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
CX NCBI_TaxID=562;
RN
RP SEQUENCE FROM N.A.
RC MEDLINE=91139577; PubMed=1995588;
RX Tao T., Bourne J.C., Blumenthal R.M.;
RT "A family of regulatory genes associated with type II restriction-
RT modification systems.";
RL J. Bacteriol. 173:1367-1375(1991).

```

DR EMBL: M63621; AAA24560.1; -.  
 FT NON TER 11 11  
 SQ SEQUENCE 11 AA; 1296 MW; 3039A71A34472AB7 CRC64;

Query Match 25.4%; Score 16; DB 2; Length 11;  
 Best Local Similarity 75.0%; Pred. No. 3.2e+04;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 PDEN 10  
 DB 4 PDLN 7

## RESULT 34

09HFN8 PRELIMINARY; PRT; 11 AA.

AC 09HFN8; 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
 DE ACP1 carrier protein (Fragment).

OS Candida rugosa (Yeast) (Candida cylindracea).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.  
 OX NCBI\_TaxID=5481;  
 RN 11  
 RP SEQUENCE FROM N.A.

RA Biasio M.;  
 RL Thesis (2000). University of Vienna, Austria.  
 DR EMBL: AJ279021; CAC08812.1; -.  
 FT NON TER 1  
 SQ SEQUENCE 11 AA; 1274 MW; D2E4CC3976C40732 CRC64;

Query Match 25.4%; Score 16; DB 3; Length 11;  
 Best Local Similarity 57.1%; Pred. No. 3.2e+04;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 YGERPPD 8  
 DB 3 YLRRQPD 9

## RESULT 35

09UAR8 PRELIMINARY; PRT; 11 AA.

AC 09UAR8; 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE Sialokin I preproprotein (Fragment).

OS Aedes aegypti (Yellowfever mosquito).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Aedes.  
 OX NCBI\_TaxID=7159;  
 RN 11  
 RP SEQUENCE FROM N.A.

RA STRAIN-Rockefeller/Red; Tissue=Salivary gland;  
 RX MEDLINE=2009025; PubMed=1620041;  
 RT Beetsen B.T.; Champagne D.E.; Coleman J.L.; Campos Y.A.; James A.A.;  
 RT "Characterization of the Sialokin I gene encoding the salivary  
 RT vasodilator of the yellow fever mosquito, Aedes aegypti.";  
 RL Insect Mol. Biol. 8:459-467 (1999).

DR EMBL: AF108100; AAD16884.1; -.  
 DR GO; GO:0007268; P:synaptic transmission; IEA.  
 DR GO; GO:0007217; P:tachykinin signaling pathway; IEA.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 FT NON TER 1  
 SQ SEQUENCE 11 AA; 1203 MW; 8BAD77C6B59C33A CRC64;

Query Match 25.4%; Score 16; DB 5; Length 11;  
 Best Local Similarity 50.0%; Pred. No. 3.2e+04;

Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 GERP 6  
 DB 3 GDXF 6

## RESULT 36

09TRW5 PRELIMINARY; PRT; 11 AA.

AC 09TRW5; 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE 25 kDa protein p25, peptide F4 (Fragment).

OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN 11  
 RP SEQUENCE.

RX MEDLINE=91372400; PubMed=1909972;  
 RA Takahashi M.; Tomizawa K.; Ishiguro K.; Sato K.; Omori A.; Sato S.;  
 RA Shiratsuchi A.; Uchida T.; Imahori K.;  
 RT "A novel brain-specific 25 kDa protein (p25) is phosphorylated by a  
 RT Ser/Thr-Pro kinase (TPK II) from tau protein kinase fractions.";  
 RL FEBS Lett. 289:37-43 (1991).  
 FT NON TER 1  
 SQ SEQUENCE 11 AA; 1276 MW; CAF72DAF65A76AA9 CRC64;

Query Match 25.4%; Score 16; DB 6; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ERF 6  
 DB 2 ERF 4

## RESULT 37

07T285 PRELIMINARY; PRT; 11 AA.

AC 07T285; 01-OCT-2003 (TREMBlrel. 25, Created)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Creatine kinase (Fragment).

OS Geochelone carbonaria (Red-footed tortoise).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Testudines; Cryptodira; Testudinoidae; Testudinidae; Geochelone.  
 OX NCBI\_TaxID=50047;  
 RN 11  
 RP SEQUENCE FROM N.A.

RA Gentile G.; Burns C.; Sezzi E.; Bergman W.; Powell J.R.; Caccione A.;  
 RT "Contrasting Patterns of Nuclear and Mitochondrial DNA Variation in  
 RT the Giant Galapagos Tortoise."  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF101746; AAM34549.1; -.  
 KW Kinase.

FT NON TER 1  
 SQ SEQUENCE 11 AA; 1356 MW; 6454ABA6733B9D4 CRC64;

Query Match 25.4%; Score 16; DB 13; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ERF 6  
 DB 3 ERF 5

```

RESULT 38
Q7T284 ID Q7T284 PRELIMINARY; PRT; 11 AA.
AC Q7T284;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Creative Kinase (Fragment).
OS Geochelone denticulata (Yellow footed tortoise).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Testudinoidea; Testudinidae; Geochelone.
OX NCBI_TaxID=101697;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=yellow2;
RA Gentile G., Burns C., Sezzi E., Bergman W., Powell J.R., Caccione A.;
RT "Contrasting Patterns of Nuclear and Mitochondrial DNA Variation in
RT the Giant Galapagos Tortoise."
RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY101747; AAM34550.1; -.
KW Kinase.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1356 MW; 6454ABA6733EB9D4 CRC64;

Query Match
Best Local Similarity 25.4%; Score 16; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ERF 6
DB 3 ERF 5

RESULT 39
Q7T283 ID Q7T283 PRELIMINARY; PRT; 11 AA.
AC Q7T283;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Creative Kinase (Fragment).
OS Geochelone pardalis (Leopard tortoise).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Testudinoidea; Testudinidae; Geochelone.
OX NCBI_TaxID=55540;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=to;
RA Gentile G., Burns C., Sezzi E., Bergman W., Powell J.R., Caccione A.;
RT "Contrasting Patterns of Nuclear and Mitochondrial DNA Variation in
RT the Giant Galapagos Tortoise."
RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY101748; AAM34551.1; -.
KW Kinase.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1356 MW; 6454ABA6733EB9D4 CRC64;

Query Match
Best Local Similarity 25.4%; Score 16; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ERF 6
DB 3 ERF 5

RESULT 40
Q7SX72 ID Q7SX72 PRELIMINARY; PRT; 11 AA.

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```

AC Q7SX72;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Creative Kinase (Fragment).
OS Geochelone chilensis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Testudinoidea; Testudinidae; Geochelone.
OX NCBI_TaxID=106216;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1864, and 8136;
RA Gentile G., Burns C., Sezzi E., Bergman W., Powell J.R., Caccione A.;
RT "Contrasting Patterns of Nuclear and Mitochondrial DNA Variation in
RT the Giant Galapagos Tortoise."
RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY101744; AAM34547.1; -.
DR EMBL; AY101745; AAM34548.1; -.
KW Kinase.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1356 MW; 6454ABA6733EB9D4 CRC64;

Query Match
Best Local Similarity 25.4%; Score 16; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ERF 6
DB 3 ERF 5

RESULT 41
Q7SX71 ID Q7SX71 PRELIMINARY; PRT; 11 AA.
AC Q7SX71;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Creative Kinase (Fragment).
OS Geochelone nigra (Galapagos giant tortoise).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Testudinoidea; Testudinidae; Geochelone.
OX NCBI_TaxID=66189;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AGOL, CAZ22, CRU1, ESP1, IG, ME4, PB3, P244, PZ6, and VA935;
RA Gentile G., Burns C., Sezzi E., Bergman W., Powell J.R., Caccione A.;
RT "Contrasting Patterns of Nuclear and Mitochondrial DNA Variation in
RT the Giant Galapagos Tortoise."
RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY101734; AAM34537.1; -.
DR EMBL; AY101735; AAM34538.1; -.
DR EMBL; AY101736; AAM34539.1; -.
DR EMBL; AY101737; AAM34540.1; -.
DR EMBL; AY101738; AAM34541.1; -.
DR EMBL; AY101739; AAM34542.1; -.
DR EMBL; AY101740; AAM34543.1; -.
DR EMBL; AY101741; AAM34544.1; -.
DR EMBL; AY101742; AAM34545.1; -.
DR EMBL; AY101743; AAM34546.1; -.
KW Kinase.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1356 MW; 6454ABA6733EB9D4 CRC64;

Query Match
Best Local Similarity 25.4%; Score 16; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ERF 6
DB 3 ERF 5

```

## RESULT 42

Q9D232 PRELIMINARY: PRT: 11 AA.

AC Q9D232.  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
DE Gag polyprotein (Fragment).  
GN GAG.

OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
NCBI\_TaxID=11676;  
RN [1]

RP SEQUENCE FROM N.A.  
RX MEDLINE=20461476; PubMed=11005867;  
RA Martinez-Picado J., Depasquale M.P., Kartsonis N., Hanna G.J.,  
RA Wong J., Finzi D., Rosenberg E., Gunthard H.F., Sutton L., Savara A.,  
RA Petropoulos C.J., Hellmann N., Walker B.D., Richman D.D.,  
RA Siliciano R., D'Aquila R.T.;  
RT "Antiretroviral resistance during successful therapy of HIV type 1  
RT infection."  
RL Proc. Natl. Acad. Sci. U.S.A. 97:10948-10953 (2000).  
DR EMBL: AF292799; AAG25407.1; -.  
KM Polyprotein.  
FT NON\_TER

SO SEQUENCE 11 AA; 1386 MW; 79DC73C0145771B4 CRC64;

Query Match 25.4%; Score 16; DB 15; Length 11;  
Best Local Similarity 60.0%; Pred. No. 3.2e+04;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 RFPD 9  
DB 4 RFPNE 8

## RESULT 43

Q81VH0 PRELIMINARY: PRT: 12 AA.

AC Q81VH0.  
DT 01-MAR-2003 (TREMBLrel. 23, Created)  
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Truncated PAX6 protein (Fragment).  
GN PAX6.

OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
NCBI\_TaxID=9606;  
RN [1]

RP SEQUENCE FROM N.A.  
RA Neethirajan G., Krishnadas S.R., Vijayalakshmi P., Sundaresan P.;  
RT "Mutation analysis in Human PAX6 gene of Aniridia."  
RT Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF548390; AAN86817.1; -.  
FT NON\_TER

SO SEQUENCE 12 AA; 1511 MW; 9E169541A67B51F1 CRC64;

Query Match 25.4%; Score 16; DB 4; Length 12;  
Best Local Similarity 66.7%; Pred. No. 3.5e+04;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 FPD 8  
DB 7 YPD 9

## RESULT 44

Q9S8F0 PRELIMINARY: PRT: 12 AA.

AC Q9S8F0.

DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE Glutathione S-transferase isoform II (EC 2.5.1.18) (Fragment).  
OS Zea mays (Maize).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
NCBI\_TaxID=4577;  
RN [1]

RP SEQUENCE.  
RX MEDLINE=95322859; PubMed=7599527;  
RA Holt D.C., Lay V.J., Clarke E.D., Dinsmore A., Jepson I., Bright S.W.,  
RA Greenland A.J.;  
RT "Characterization of the safener-induced glutathione S-transferase  
RT isoform II from maize."  
RL Planta 196:295-302 (1995).  
DR GO: 0004364; F:glutathione transferase activity; IEA.

SO SEQUENCE 12 AA; 1382 MW; C28977FF65975B05D CRC64;

Query Match 25.4%; Score 16; DB 10; Length 12;  
Best Local Similarity 66.7%; Pred. No. 3.5e+04;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 IYG 3  
DB 1 YYG 3

## RESULT 45

Q88577 PRELIMINARY: PRT: 12 AA.

AC Q88577.  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds  
DE (Fragment).  
OS Theiler's encephalomyelitis virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;  
OC Cardiovirus.

NCBI\_TaxID=12124;  
RN [1]

RP SEQUENCE FROM N.A.  
RX MEDLINE=92194426; PubMed=1548749;  
RA Pritchard A.E., Galenoff M.A., Simpson S., Jensen K., Lipson H.L.;  
RT "A single base deletion in the 5' noncoding region of Theiler's virus  
RT attenuates neurovirulence."  
RT J. Virol. 66:1951-1958 (1992).  
DR EMBL: M80885; AAA73156.1; -.  
FT NON\_TER

SO SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match 25.4%; Score 16; DB 12; Length 12;  
Best Local Similarity 66.7%; Pred. No. 3.5e+04;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 FPD 8  
DB 7 YPD 9

Search completed: August 30, 2004, 10:55:24  
Job time: 13.5912 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:09 ; Search time 1.69527 Seconds  
(without alignments)  
302.211 Million cell updates/sec

Title: US-09-720-469a-6  
Perfect score: 63  
Sequence: 1 IYGERFPDENF 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 585

Minimum DB seq length: 8  
Maximum DB seq length: 14

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	39.7	10	1	SLAP_BACTG
2	23	36.5	10	1	URA7_HUMAN
3	21	33.3	11	1	COXA_CANFA
4	21	33.3	11	1	TKN4_PSECU
5	21	33.3	12	1	FIF1_SARBU
6	20	31.7	10	1	FAR7_MACRS
7	20	31.7	14	1	LPER_BACLI
8	19	30.2	9	1	FAR2_MACRS
9	19	30.2	9	1	FAR3_MACRS
10	19	30.2	11	1	ERG_CLOPA
11	18	28.6	8	1	FAR1_PENNO
12	18	28.6	8	1	FAR3_HOMAM
13	18	28.6	9	1	UPA3_HUMAN
14	18	28.6	10	1	PNEU_RAT
15	18	28.6	10	1	PR02_BOVIN
16	18	28.6	11	1	TKN1_PSECU
17	18	28.6	11	1	TKN1_PSECU
18	18	28.6	11	1	TKN1_PSECU
19	18	28.6	12	1	TKN2_PSECU
20	18	28.6	13	1	PSBP_PHYPA
21	18	28.6	13	1	PSBP_PHYPA
22	18	28.6	13	1	PSBP_PHYPA
23	18	28.6	14	1	MARI_ALTPP
24	17	27.0	8	1	FAR1_PANRE
25	17	27.0	9	1	FAR2_PANRE
26	17	27.0	10	1	UPA8_HUMAN
27	17	27.0	11	1	UPA8_HUMAN
28	17	27.0	11	1	LSKP_PENAM
29	17	27.0	13	1	ADFB_TENNO
30	17	27.0	14	1	NSK2_SARBU
31	17	27.0	14	1	TKN1_SCHGR
32	17	27.0	14	1	UC04_MAIZE
33	16	25.4	8	1	ATL1_CYPDO

34	16	25.4	8	1	FAR7_ASCSU	P43171 ascaris suu
35	16	25.4	9	1	FAR1_CALVO	P41856 calliphora
36	16	25.4	9	1	FAR2_CALVO	P41857 calliphora
37	16	25.4	9	1	FAR3_CALVO	P41858 calliphora
38	16	25.4	9	1	FRP1_SARBU	P83350 sarcophaga
39	16	25.4	9	1	TKL1_CALVO	P41517 calliphora
40	16	25.4	9	1	TKL1_CALVO	P41517 calliphora
41	16	25.4	10	1	PORB_MERTM	P80901 methanobact
42	16	25.4	10	1	PCPK_FASHE	P80525 fasciola he
43	16	25.4	10	1	TKL2_LOCOM	P16224 locusta mig
44	16	25.4	10	1	TKL3_LOCOM	P30249 locusta mig
45	16	25.4	10	1	TKS1_AEDAE	P42634 aedes aegypt

## ALIGNMENTS

RESULT 1  
SLAP\_BACTG  
ID SLAP\_BACTG STANDARD; PRT; 10 AA.  
AC P49325;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last annotation update)  
DE S-layer protein (Surface layer protein) (Fragment).  
OS Bacillus thuringiensis (subsp. galleriae).  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=29338;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=NRRL 4045;  
RX MEDLINE=80078111; PubMed=2592346;  
RA Luckey M.D., Beveridge T.O.,  
RT "Characterization of a dynamic S layer on Bacillus thuringiensis.",  
RL J. Bacteriol. 171:6556-6667(1989).  
CC -1- FUNCTION: The S-layer is a paracrystalline mono-layered assembly  
CC of proteins which coat the surface of bacteria.  
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A  
CC S-LAYER WITH OBLIQUE (P2) SYMMETRY.  
DR PIR; A60476; A60476.  
KW Cell wall; S-layer.  
FT NON TER  
SQ SEQUENCE 10 AA; 1080 MW; 57AECAAB769D1A3 CRC64;  
Query Match 39.7%; Score 25; DB 1; Length 10;  
Best Local Similarity 66.7%; Pred. No. 85;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 3 GERFPD 8  
Db 2 GRTFPD 7  
RESULT 2  
URA7\_HUMAN  
ID URA7\_HUMAN STANDARD; PRT; 10 AA.  
AC P34950;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Unknown protein from 2D-page of red blood cells (Spot 2D-006H0)  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Erythrocyte;  
RA Golaz O., Hughes G.J., Frutiger S., Paquet N., Balroch A.,  
RA Pasquali C., Sanchez J.-C., Tissot J.-D., Appel R.D., Walzer C.,  
RA Balant L., Hochstrasser D.F.;  
RL Submitted (FEB-1994) to Swiss-Prot.

CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
 CC protein is: 4.77, its MW is: 26 kDa.  
 DR SWISS-2DPAGE; P34990; HUMAN.  
 FT NON\_TER 10  
 SQ SEQUENCE 10 AA; 1161 MW; F72D829C44B1871 CRC64;  
 Query Match 36.5%; Score 23; DB 1; Length 10;  
 Best Local Similarity 57.1%; Pred. No. 2e+02;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 YGERPDP 8  
 DB 3 HGENFXD 9

RESULT 3  
 ID COXA\_CANFA STANDARD; PRT; 11 AA.  
 AC P99501;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Cytochrome c oxidase polypeptide Va (EC 1.9.3.1) (Fragment).  
 GN COXA5A.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Heart;  
 RX MEDLINE=98163340; PubMed=9504812;  
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;  
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of  
 RT dog heart proteins";  
 RL Electrophoresis 18:2795-2802(1997).  
 CC -1- FUNCTION: This is the heme A-containing chain of cytochrome c  
 CC oxidase, the terminal oxidase in mitochondrial electron transport.  
 CC -1- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome  
 CC c + 2 H(2)O.  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.  
 CC -1- SIMILARITY: Belongs to the cytochrome c oxidase Va family.  
 DR HSC-2DPAGE; P99501; DOG.  
 DR InterPro: IPR003204; Cyt\_c\_ox5a.  
 DR Pfam: PF02284; COX5A; 1\_\_ox5a.  
 KW Oxidoreductase; Heme; Mitochondrion; Inner membrane.  
 FT NON\_TER 11  
 SQ SEQUENCE 11 AA; 1274 MW; 910B35C5B1AB1F5 CRC64;

Query Match 33.3%; Score 21; DB 1; Length 11;  
 Best Local Similarity 40.0%; Pred. No. 5.1e+02;  
 Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 2 YGERPDP 11  
 DB 2 HSHSHDEBF 11

RESULT 4  
 ID TKN4\_PSEGU STANDARD; PRT; 11 AA.  
 AC P42989;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Substance P-like peptide I (PS-SPI).  
 OS Pseudoputryne guentheri (Guenther's toadlet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Myobatrachidae;  
 OC NCBI\_TaxID=30349;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE=Skin secretion;  
 RX MEDLINE=90287814; PubMed=2356157;  
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
 RA Roberts J.D., Melchiorri P., Erspamer V.;  
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
 RT the Australian frog Pseudoputryne guentheri";  
 RL Peptides 11:299-304(1990).  
 CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Skin.  
 CC -1- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; E60409; E60409.  
 DR InterPro: IPR002040; Tachy\_Neurokinin.  
 DR InterPro: IPR008215; Tachykinin.  
 DR Pfam: PF02202; Tachykinin; 1.  
 DR SMART: SM00203; TK; 1.  
 DR PROSITE: PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyroglutamate carboxylic acid.  
 FT MOD\_RES 1  
 FT MOD\_RES 1  
 FT MOD\_RES 1  
 SQ SEQUENCE 11 AA; 1294 MW; 3A247C2CC9CB1AB7 CRC64;

Query Match 33.3%; Score 21; DB 1; Length 11;  
 Best Local Similarity 80.0%; Pred. No. 5.1e+02;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 7 PDENF 11  
 DB 4 PDEPF 8

RESULT 5  
 ID FIF1\_SARBU STANDARD; PRT; 12 AA.  
 AC P83349;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Neb-FIRamide 1.  
 OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 OC Sarcophagidae; Sarcophaga.  
 OX NCBI\_TaxID=7385;  
 RN [1]  
 RP SEQUENCE, AMIDATION, AND FUNCTION.  
 RC TISSUE=CNS;  
 RX MEDLINE=22342733; PubMed=12438685;  
 RA Meusen T., Mertens I., Clynen E., Baggerman G., Nichols R.,  
 RA Neuman R.J., Huybrechts R., De Loof A., Schoofs L.;  
 RT "Identification in Drosophila melanogaster of the invertebrate G  
 RT protein-coupled FMRFamide receptor";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).  
 CC -1- FUNCTION: Has modulatory actions at skeletal neuromuscular  
 CC junctions.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)  
 CC family.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 12  
 FT MOD\_RES 12  
 SQ SEQUENCE 12 AA; 1369 MW; 2DC45519C14B5A7 CRC64;

Query Match 33.3%; Score 21; DB 1; Length 12;  
 Best Local Similarity 60.0%; Pred. No. 5.6e+02;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 7 PDENF 11  
 DB 5 PSDNF 9



RESULT 6  
FAR7\_MACRS STANDARD; PRT; 10 AA.  
ID FAR7\_MACRS STANDARD; PRT; 10 AA.  
AC P83280;  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DE FMRFamide-like neuropeptide FL77 (GyDKNFLRF-amide).  
OS Macrobrachium rosenbergii (Giant fresh water prawn).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;  
OC Palaemonoidea; Palaemonidae; Macrobrachium.  
CX NCBI\_TaxID=79674;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Eyestalk;  
RX MEDLINE=21107394; PubMed=1179812;  
RA Sithigorngul P., Sarathongkum W., Longyant S., Panchan N.,  
RA Sithigorngul W., Petson A.;  
RT "Three more novel FMRFamide-like neuropeptide sequences from the  
RT eyestalk of the giant freshwater prawn Macrobrachium rosenbergii.",  
RL Peptides 22:191-197(2001).  
CC -1- MASS SPECTROMETRY: MW=1244.9; METHOD=MALDI.  
CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)  
CC family.  
CC GO:GO:0007218; P:neuropeptide signaling pathway; IDA.  
DR Neuropeptide; Amidation.  
KM MOD\_RES 10 10 AMIDATION.  
SQ SEQUENCE 10 AA; 1244 MW; 3CFB9C29C4540A8 CRC64;  
Query Match 31.7%; Score 20; DB 1; Length 10;  
Best Local Similarity 75.0%; Pred. No. 7.1e+02;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 2 YGER 5  
DB 2 YGDR 5  
RESULT 7  
LPER\_BACLI STANDARD; PRT; 14 AA.  
ID LPER\_BACLI STANDARD; PRT; 14 AA.  
AC Q04303;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Erythromycin resistance leader peptide (23S rRNA methylase leader  
DE peptide).  
OS Bacillus licheniformis, and  
OS Bacillus anthracis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
CX NCBI\_TaxID=1402, 1392;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC SPECIES=B.licheniformis;  
RX MEDLINE=84245158; PubMed=6429477;  
RA Gryczan T., Israel-Riches M., del Bue M., Dubnau D.;  
RT "DNA sequence and regulation of ermD, a macrolide-lincosamide-  
RT streptogramin B resistance element from Bacillus licheniformis";  
RL Mol. Genet. 194:349-356(1984).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC SPECIES=B.licheniformis; STRAIN=EXR-1;  
RX MEDLINE=91310580; PubMed=1713206;  
RA Kwak J.-K., Choi E.-C., Weisblum B.;  
RT "Transcriptional attenuation control of ermK, a  
RT macrolide-lincosamide-streptogramin B resistance determinant from  
RT Bacillus licheniformis";  
RL J. Bacteriol. 173:4725-4735(1991).  
RN [3]  
RP SEQUENCE FROM N.A.

RC SPECIES=B.anthraxis; STRAIN=590;  
RX MEDLINE=93232776; PubMed=8473865;  
RA Kim H.-S., Choi E.-C., Kim B.-K.;  
RT "A macrolide-lincosamide-streptogramin B resistance determinant from  
RT Bacillus anthracis 590: cloning and expression of ermJ";  
RL J. Gen. Microbiol. 139:601-607(1993).  
CC -1- FUNCTION: THIS PEPTIDE IS INVOLVED IN THE CONTROL MECHANISM OF  
CC THE SYNTHESIS OF THE MACROLIDE-LINCOSAMIDE-STREPTOGRAMIN B  
CC RESISTANCE PROTEIN. IT ACTS AS A TRANSCRIPTIONAL ATTENUATOR.  
CC -----  
CC THIS SWISS-PROT entry is copyrighted. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; L08389; AAA22596.1; -  
DR EMBL; M29832; AAA22598.1; -  
DR PIR; A42473; A42473.  
KM Antibiotic resistance; Leader peptide.  
SQ SEQUENCE 14 AA; 1732 MW; 5D1138B59F32BD07 CRC64;  
Query Match 31.7%; Score 20; DB 1; Length 14;  
Best Local Similarity 66.7%; Pred. No. 1e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 5 RFPDEN 10  
DB 8 RFPETL 13  
RESULT 8  
FAR2\_MACRS STANDARD; PRT; 8 AA.  
ID FAR2\_MACRS STANDARD; PRT; 8 AA.  
AC P83275;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DE FMRFamide-like neuropeptide FL72 (ADKNFLRF-amide).  
OS Macrobrachium rosenbergii (Giant fresh water prawn).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;  
OC Palaemonoidea; Palaemonidae; Macrobrachium.  
CX NCBI\_TaxID=79674;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Eyestalk;  
RX MEDLINE=21107394; PubMed=1179812;  
RA Sithigorngul P., Sarathongkum W., Jaidechoy S., Longyant S.,  
RA Sithigorngul W.;  
RT "Novel FMRFamide-like neuropeptides from the eyestalk of the giant  
RT freshwater prawn Macrobrachium rosenbergii";  
RL Comp. Biochem. Physiol. 120B:587-595(1998).  
CC -1- MASS SPECTROMETRY: MW=1009.4; METHOD=MALDI.  
CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)  
CC family.  
CC GO:GO:0007218; P:neuropeptide signaling pathway; TAS.  
DR Neuropeptide; Amidation.  
KM MOD\_RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA; 1010 MW; 9CD40729C4433AAD CRC64;  
Query Match 30.2%; Score 19; DB 1; Length 8;  
Best Local Similarity 75.0%; Pred. No. 1.4e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 8 DENF 11  
DB 2 DKNF 5  
RESULT 9  
FAR3\_MACRS

ID PAR3 MACRS STANDARD; PRT; 9 AA.  
AC P83276;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE FMRamide-like neuropeptide FLP3 (NYDKNPLRF-amide).  
OS Macrobrachium rosenbergii (Giant fresh water prawn).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;  
OC Palaemonoidae; Palaemonidae; Macrobrachium.  
NCBI\_TaxID=79674;  
RN [1]  
RN SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Eyestalk;  
RA Sitihingnui P., Sarathongkum W., Jaidechoe S., Longyant S.,  
RA Sitihingnui W.;  
RT "Novel FMRamide-like neuropeptides from the eyestalk of the giant  
freshwater prawn Macrobrachium rosenbergii.";  
RL Comp. Biochem. Physiol. 120B:587-595(1998).  
CC -1- MASS SPECTROMETRY: MW=1215.4; METHOD=MALDI.  
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)  
family.  
DR GO: GO:0007218; P:neuropeptide signaling pathway; TAS.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 9 AA; 1216 MW; 18220729C4433AB CRC64;  
SQ SEQUENCE 9 AA; 1216 MW; 18220729C4433AB CRC64;  
Query Match 30.2%; Score 19; DB 1; Length 9;  
Best Local Similarity 75.0%; Pred. No. 1.4e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 8 DENF 11  
DB 3 DKNF 6  
RESULT 10  
ERG\_CLOPA STANDARD; PRT; 11 AA.  
ID P81350;  
AC 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Elongation factor G (EF-G) (CP 5) (Fragment).  
CN FUSA  
OS Clostridium pasteurianum.  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
OC Clostridium.  
OX NCBI\_TaxID=1501;  
RN [1]  
RN SEQUENCE.  
RC STRAIN=MS;  
RX MEDLINE=98291870; PubMed=9629918;  
RA Flengstrand R., Skjeldal L.;  
RT "Two-dimensional gel electrophoresis separation and N-terminal  
sequence analysis of proteins from Clostridium pasteurianum WS.";  
RL Electrophoresis 19:802-806(1998).  
CC -1- FUNCTION: This protein promotes the GTP-dependent translocation of  
the nascent protein chain from the A-site to the P-site of the  
ribosome.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -1- SIMILARITY: Belongs to the GTP-binding elongation factor family.  
DE InterPro: IPR000795; EF\_GTPbind.  
DR PROSITE: PS00301; EFACITOR GTP: PARTIAL.  
KW Elongation factor; Protein biosynthesis; GTP-binding.  
FT NON\_TER 11  
SQ SEQUENCE 11 AA; 1337 MW; 412E71F1D9C33B17 CRC64;  
Query Match 30.2%; Score 19; DB 1; Length 11;  
Best Local Similarity 42.9%; Pred. No. 1.2e+03;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 REPDENF 11  
DB 1 KYPLEKF 7  
RESULT 11  
ID FARP1 PENMO STANDARD; PRT; 8 AA.  
AC P83316;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE FMRamide-like neuropeptide FLP2 (GDRNPLRF-amide).  
OS Penaeus monodon (penaeid shrimp).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;  
OC Penaeidae; Penaeus.  
OX NCBI\_TaxID=6687;  
RN [1]  
RN SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Eyestalk;  
RA Sitihingnui P., Pupuem J., Krungkasem C., Longyant S.,  
RA Chaitisangkura P., Sitihingnui W., Petson A.;  
RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk  
of the giant tiger prawn Penaeus monodon.";  
RL Comp. Biochem. Physiol. 131B:325-337(2002).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- MASS SPECTROMETRY: MW=1024.8; METHOD=MALDI.  
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)  
family.  
DR GO: GO:0007218; P:neuropeptide signaling pathway; TAS.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 8 AA; 1024 MW; 72D40729C4540A8 CRC64;  
SQ SEQUENCE 8 AA; 1024 MW; 72D40729C4540A8 CRC64;  
Query Match 28.6%; Score 18; DB 1; Length 8;  
Best Local Similarity 75.0%; Pred. No. 1.4e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 8 DENF 11  
DB 2 DKNF 5  
RESULT 12  
ID FARP3 HOMAM STANDARD; PRT; 8 AA.  
AC P41486;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE FMRamide-like neuropeptide 3 (FLI 3) (F2).  
OS Homarus americanus (American lobster).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;  
OC Nephropoidea; Nephropidae; Homarus.  
OX NCBI\_TaxID=6706;  
RN [1]  
RN SEQUENCE.  
RC TISSUE=Pericardial organs;  
RX MEDLINE=88116164; PubMed=3429714;  
RA Trimmer B.A., Koblitz L.A., Kravitz E.A.;  
RT "Purification and characterization of FMRamide-like immunoreactive  
substances from the lobster nervous system: isolation and sequence  
analysis of two closely related peptides.";  
RL J. Comp. Neurol. 265:16-26(1987).  
CC -1- MISCELLANEOUS: Pericardial organs release this peptide with 100 mM  
potassium in the presence of calcium.  
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)  
family.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 8 AA; 1024 MW; 72D40729C4540A8 CRC64;

SQ SEQUENCE 8 AA; 1054 MW; C6D40729C4540AB5 CRC64;

Query Match 28.6%; Score 18; DB 1; Length 8;  
Best Local Similarity 75.0%; Pred. No. 1.4e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 8 DENF 11  
DB 2 DRNF 5

RESULT 13

UPA3\_HUMAN STANDARD; PRT; 9 AA.

AC P30089;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Unknown protein from 2D-page of plasma (Spot 11) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Plasma;  
RA MEDLINE=93092937; PubMed=1459097;  
RA Hughes G.U., Frutiger S., Paquet N., Ravier F., Pasquall C.,  
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,  
RA Hochstrasser D.F.;  
RT "Plasma protein map: an update by microsequencing.";  
RL Electrophoresis 13:707-714(1992).  
CC -I- MICELLANEOUS: On the 2D-gel the determined pI of this unknown  
CC protein is: 4.6, its MW is: 46 kDa.  
DR SWISS-2DPAGE; P30089; HUMAN.  
FT NON\_TER  
FT 1  
SQ SEQUENCE 9 AA; 1056 MW; 26F2B1BAF769C737 CRC64;

Query Match 28.6%; Score 18; DB 1; Length 9;  
Best Local Similarity 50.0%; Pred. No. 1.4e+05;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 6 FPDENF 11  
DB 4 FPDTF 9

RESULT 14

PNEU\_RAT STANDARD; PRT; 10 AA.

AC P21956;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Pneumadin (Pm).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RC TISSUE=Lung;  
RA MEDLINE=9110910; PubMed=2274691;  
RA Batra V.K., Mathur M., Mir S.A., Kapoor R., Kumar M.A.;  
RT "Pneumadin: a new lung peptide which triggers antidiuretic.";  
RL Regul. Pept. 30:77-87(1990).  
CC -I- FUNCTION: This antidiuretic peptide triggers the release of ADH.  
DR PIR; A33143; A33143.  
KM Amidation.  
FT MOD\_RES  
FT 10  
SQ SEQUENCE 10 AA; 1048 MW; 641D0DDA723276B CRC64;

Query Match 28.6%; Score 18; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 YGE 4  
DB 1 YGE 3

RESULT 15

RT02\_BOVIN STANDARD; PRT; 10 AA.

AC P29253;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Mitochondrial 28S ribosomal protein S2 (MRP-S2) (Fragment).  
GN MRP52.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Liver;  
RA MEDLINE=21276436; PubMed=11279123;  
RA Koc E.C., Burkhardt W., Blackburn K., Noseley A., Spremulli L.L.;  
RT "The small subunit of the mammalian mitochondrial ribosome:  
RT identification of the full complement of ribosomal proteins present.";  
RL J. Biol. Chem. 276:19363-19374(2001).  
CC -I- SUBUNIT: Component of the mitochondrial ribosome small subunit  
CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.  
CC -I- SIMILARITY: Belongs to the S2P family of ribosomal proteins.  
DR InterPro; IPR001865; Ribosomal\_S2.  
DR PROSITE; PS00962; RIBOSOMAL\_S2\_1; PARTIAL.  
KM Ribosomal protein; Mitochondrion.  
FT NON\_TER  
FT 1  
SQ SEQUENCE 10 AA; 1246 MW; 6A7A6679C04B476B CRC64;

Query Match 28.6%; Score 18; DB 1; Length 10;  
Best Local Similarity 60.0%; Pred. No. 1.6e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 YGER 5  
DB 6 IFGR 10

RESULT 16

TKN1\_PSEGU STANDARD; PRT; 11 AA.

AC P42986;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Kaeslin-like peptide K-1 (Pg-K1).  
OS Pseudophryne guentheri (Guenther's toadlet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
OC Myobatrachinae; Pseudophryne.  
OX NCBI\_TaxID=30349;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RA MEDLINE=90267814; PubMed=2356157;  
RA Simmaco W., Severini C., de Biase D., Barra D., Bossa F.,  
RA Roberts J.D., Melchiorri P., Bispham V.;  
RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
RT the Australian frog Pseudophryne guentheri.";  
RL Peptides 11:299-304(1990).

CC -|- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -|- SUBCELLULAR LOCATION: Secreted.  
 CC -|- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR: B60409; B60409.  
 DR InterPro: IPR002040; Tachy Neurokinin.  
 DR InterPro: IPR008215; Tachykinin.  
 DR Pfam: PF02202; Tachykinin; 1.  
 DR SMART: SM00203; TK; 1.  
 DR PROSITE: PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1269 MW; 3DBATC37C9C1AB7 CRC64;

Query Match 28.6%; Score 18; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PDE 9  
 |||  
 Db 4 PDE 6

RESULT 17  
 ID\_TKN1\_UPERU STANDARD; PRT; 11 AA.  
 AC P06612;  
 DT 01-NOV-1998 (Rel. 08, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Uperolein.  
 OS Uperoleia rugosa (Wrinkled toadlet).  
 DR PROSITE: PS00267; TACHYKININ; 1.  
 KW Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Myobatrachidae;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Myobatrachidae;  
 CC Myobatrachinae; Uperoleia.  
 OK NCBI\_Taxid=8368;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=7513127; PubMed=1120493;  
 RA Anastasi A., Erspamer V., Endean R.;  
 RT "Structure of uperolein, a physalaemin-like endecapeptide occurring  
 in the skin of Uperoleia rugosa and Uperoleia marmorata.";  
 RL Experientia 31:394-395(1975).  
 CC -|- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -|- SUBCELLULAR LOCATION: Secreted.  
 CC -|- TISSUE SPECIFICITY: Skin.  
 CC -|- SIMILARITY: Belongs to the tachykinin family.  
 DR InterPro: IPR002040; Tachy Neurokinin.  
 DR InterPro: IPR008215; Tachykinin.  
 DR Pfam: PF02202; Tachykinin; 1.  
 DR SMART: SM00203; TK; 1.  
 DR PROSITE: PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1252 MW; 3Z867C3B59CDD457 CRC64;

Query Match 28.6%; Score 18; DB 1; Length 11;  
 Best Local Similarity 75.0%; Pred. No. 1.8e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 7 PDEN 10  
 |||

Db 2 PDEN 5

RESULT 18  
 ID\_TKN2\_PSEGU STANDARD; PRT; 11 AA.  
 AC P42967;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Kassinin-like peptide K-II (PG-KII).  
 OS Pseudophryne guentheri (Guenther's toadlet).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Myobatrachidae;  
 CC Myobatrachinae; Pseudophryne.  
 OK NCBI\_Taxid=30349;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=90287814; PubMed=2356157;  
 RA Stimmco M., Severini C., de Biase D., Barra D., Boesa F.,  
 RA Roberts U.D., Melchiorri P., Erspamer V.;  
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
 the Australian frog Pseudophryne guentheri.";  
 RL Peptides 11:299-304(1990).  
 CC -|- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -|- SUBCELLULAR LOCATION: Secreted.  
 CC -|- TISSUE SPECIFICITY: Skin.  
 CC -|- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR: C60409; C60409.  
 DR InterPro: IPR002040; Tachy Neurokinin.  
 DR InterPro: IPR008215; Tachykinin.  
 DR Pfam: PF02202; Tachykinin; 1.  
 DR SMART: SM00203; TK; 1.  
 DR PROSITE: PS00267; TACHYKININ; 1.  
 KW Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Myobatrachidae;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1246 MW; 3A247C37C9C1AB7 CRC64;

Query Match 28.6%; Score 18; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 7 PDE 9  
 |||  
 Db 4 PDE 6

RESULT 19  
 ID\_PSP3\_PHYPA STANDARD; PRT; 12 AA.  
 AC P80662;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Oxygen-evolving enhancer protein II (Fragment).  
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;  
 CC Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrellia.  
 OK NCBI\_Taxid=3218;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Protonema;  
 RX MEDLINE=97275459; PubMed=9129336;  
 RA Kasten B., Buck F., Nuske J., Reski R.;  
 RT "Cytokinin affects nuclear- and plastome-encoded energy-converting  
 plastid enzymes.";

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RL Plantae 201:261-272(1997).
CC -1- FUNCTION: May be involved in the regulation of photosystem II.
CC -1- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane; associated
CC with the photosystem II complex.
CC -1- INDUCTION: By light.
CC -1- SIMILARITY: Belongs to the psbp family.
CC Photosynthesis; Photosystem II; Chloroplast; Thylakoid; Membrane;
CC Multigene family.
KW NON TER
FT 12
SQ SEQUENCE 12 AA; 1182 MW; 8D2B0D54D7C4DC5 CRC64;

Query Match 28.6%; Score 18; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGE 4
DB 2 YGE 4

RESULT 20
NP3_LYMST STANDARD; PRT; 13 AA.
AC P80180;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Lymnaea-DF-amide 3.
OS Lymnaea stagnalis (Great pond snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Bascommatophora;
OC Lymnaeidae; Lymnaeidae; Lymnaea.
OX NCBI_TaxID=6523;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=93238777; PubMed=8477756;
RA Johsen A.H., Rehfeld J.F.;
RT "Lymnaea stagnalis, a new family of neuropeptides from the pond snail,
RT Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in
RT invertebrates?";
RL Eur. J. Biochem. 213:875-879(1993).
CC -1- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CCK) FAMILY.
DR PIR: S32473; S32473.
KW Neuropeptide; Amidation.
FT MOD_RES 13
FT UNRES 12
SQ SEQUENCE 13 AA; 1462 MW; 9CA07BA3F5D5B865 CRC64;

Query Match 28.6%; Score 18; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.2e+03;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 IYGERPD 8
DB 5 ISGSAFSD 12

RESULT 21
PSBP_PINPS STANDARD; PRT; 13 AA.
AC P81668;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Oxygen-evolving enhancer protein 2 (OEE2) (23 kDa subunit of oxygen
DE evolving system of photosystem II) (Fragment).
KW PSBP.
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.

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RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Plomieu C., Bauw G., Dubos C., Bahrmann N., Kremer A.,
RA Frigerio J.-M., Plomieu C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -1- FUNCTION: May be involved in the regulation of photosystem II.
CC -1- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane; associated
CC with the photosystem II complex (by similarity).
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this protein
CC (spot N179) is: 5.9, its MW is: 22 kDa.
CC -1- SIMILARITY: Belongs to the psbp family.
KW Photosynthesis; Photosystem II; Chloroplast; Thylakoid; Membrane.
FT NON TER 13
SQ SEQUENCE 13 AA; 1294 MW; C6772B0D54D7C44D CRC64;

Query Match 28.6%; Score 18; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGE 4
DB 2 YGE 4

RESULT 22
MARI_ALTPSP STANDARD; PRT; 14 AA.
AC P29399;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Marinostatin C-2 (Marinostatin C-1; Marinostatin D).
OS Alteromonas sp. (Strain B-10-31).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Alteromonadaceae; Alteromonas.
OX NCBI_TaxID=29456;
RN [1]
RP SEQUENCE AND ACTIVE SITE.
RX MEDLINE=92176155; PubMed=1794974;
RA Takano R., Imada C., Kamet K., Hara S.;
RT "The reactive site of marinostatin, a proteinase inhibitor from
RT marine Alteromonas sp. B-10-31.";
RL J. Biochem. 110:856-858(1991).
CC -1- FUNCTION: INHIBITS SUBTILISIN, CHYMOTRYPSIN, AND ELASTASE, BUT
CC NOT TRYPSIN.
KW Serine protease inhibitor; Pyrrolidone carboxylic acid.
FT PEPTIDE 1
FT PEPTIDE 14
FT PEPTIDE 3
FT MOD_RES 4
FT MOD_RES 1
FT ACT_SITE 1
SQ SEQUENCE 14 AA; 1644 MW; 6E7CEBF92EF32E44 CRC64;

Query Match 28.6%; Score 18; DB 1; Length 14;
Best Local Similarity 33.3%; Pred. No. 2.4e+03;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 RFPPDEN 10
DB 7 RYPSDD 12

RESULT 23
FARI_PANRE STANDARD; PRT; 8 AA.
AC P41872;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFamide-like neuropeptide PFI (SDPNFLRF-amide).
OS Panagrellus redivivus.

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OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
 OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.  
 OX NCBI\_TaxId=6233;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=93027659; PubMed=1408999;  
 RA Geary T.G., Price D.A., Bowman J.W., Winterrowd C.A., Mackenzie C.D.,  
 RT "Two FMRamide-like peptides from the free-living nematode  
 Panagrellus redivivus";  
 RL Peptides 13:209-214(1992).  
 CC CC  
 CC -1- TISSUE SPECIFICITY: Nerve cords and paired groups of cells located  
 CC caudally to the base of the pharynx.  
 CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)  
 CC family.  
 KM Neuropeptide; Amidation.  
 FT MOD RES  
 SQ SEQUENCE 8 AA; 995 MW; C6D40729C4576AB5 CRC64;

Query Match 27.0%; Score 17; DB 1; Length 8;  
 Best Local Similarity 75.0%; Pred. No. 1.4e+05;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 DENF 11  
 DB 2 DENF 5

RESULT 24  
 PAR2\_PANRE STANDARD; PRT; 9 AA.  
 AC P41873;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE FMRamide-like neuropeptide PF2 (SADPNFLRF-amide).  
 OS Panagrellus redivivus.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
 OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.  
 OX NCBI\_TaxId=6233;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=93027659; PubMed=1408999;  
 RA Geary T.G., Price D.A., Bowman J.W., Winterrowd C.A., Mackenzie C.D.,  
 RT "Two FMRamide-like peptides from the free-living nematode  
 Panagrellus redivivus";  
 RL Peptides 13:209-214(1992).  
 CC CC  
 CC -1- FUNCTION: Myoactive.  
 CC -1- TISSUE SPECIFICITY: Nerve cords and paired groups of cells located  
 CC caudally to the base of the pharynx.  
 CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)  
 CC family.  
 KM Neuropeptide; Amidation.  
 FT MOD RES  
 SQ SEQUENCE 9 AA; 1066 MW; DA0B0729C4576AAD CRC64;

Query Match 27.0%; Score 17; DB 1; Length 9;  
 Best Local Similarity 75.0%; Pred. No. 1.4e+05;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 DENF 11  
 DB 3 DENF 6

RESULT 25  
 PAR4\_CALVO STANDARD; PRT; 9 AA.  
 AC P41859;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Calliphramide 4.  
 OS Calliphora vomitoria (Blue blowfly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 OC Calliphoridae; Calliphora.  
 OX NCBI\_TaxId=27454;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Thoracic ganglion;  
 RX MEDLINE=9219611; PubMed=1549595;  
 RA Dave H., Johnson A.H., Sewell J.C., Scott A.G., Orchard I.,  
 RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2  
 neuropeptides (designated calliphramides) from the blowfly  
 Calliphora vomitoria";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).  
 CC CC  
 CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)  
 CC family.  
 DR PIR; D41979; DA1978.  
 KM Neuropeptide; Amidation.  
 FT MOD RES  
 SQ SEQUENCE 9 AA; 1182 MW; 31730699CAB6D457 CRC64;

Query Match 27.0%; Score 17; DB 1; Length 9;  
 Best Local Similarity 40.0%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 7 PDENF 11  
 DB 2 PNODF 6

RESULT 26  
 UP88\_HUMAN STANDARD; PRT; 10 AA.  
 ID UP88\_HUMAN  
 AC P30094;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Unknown protein from 2D-page of plasma (Spot 34) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Plasma;  
 RX MEDLINE=93092937; PubMed=1459097;  
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,  
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,  
 RT "Plasma protein map: an update by microsequencing";  
 RL Electrophoresis 13:707-714(1992).  
 CC CC  
 CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
 CC protein is: 7.2, its MW is: 16 KDa.  
 DR SWISS-2DPAGE; P30094; HUMAN.  
 CC CC  
 CC VARIANTS 4 4 S->H.  
 FT NON\_TER  
 FT VARIANTS 1 1 /FTID=VAR\_000003.  
 FT NON\_TER  
 FT NON\_TER  
 SQ SEQUENCE 10 AA; 977 MW; 2EA6B0C77AB25B8 CRC64;

Query Match 27.0%; Score 17; DB 1; Length 10;  
 Best Local Similarity 42.9%; Pred. No. 2.5e+03;  
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IYGERFP 7  
 DB 1 IYGSCKP 7

RESULT 27

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LSK1_LEUMA
ID LSK1_LEUMA STANDARD; PRT; 11 AA.
AC P04428;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Leucosulfakinin-1 (LSK-1).
OS Leucophaea mederae (Madaira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OC NCBI_TaxID=69388;
RN [1]
RP SEQUENCE.
RX MEDLINE=86315858; PubMed=3749893;
RA Nachman R.J., Holman G.M., Haddon W.F., Ling N.;
RT "Leucosulfakinin, a sulfated insect neuropeptide with homology to
RT gastrin and cholecystokinin."
RL Science 234:71-73(1986).
CC -1- FUNCTION: Change the frequency and amplitude of contractions of
CC the hindgut. Inhibits muscle contraction of hindgut.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR PIR; A01622; GMRCL.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Hormone; Amidation; Sulfation.
FT MOD RES 6
FT MOD RES 11
FT MOD RES 11
SQ SEQUENCE 11 AA; 1459 MW; 7E4B0680E86B5AAB CRC64;

Query Match
Best Local Similarity 27.0%; Score 17; DB 1; Length 11;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPD 8
Db 1 ERFDD 5

RESULT 28
LSKP_PERAM STANDARD; PRT; 11 AA.
ID LSKP_PERAM STANDARD; PRT; 11 AA.
AC P36883;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Perisulfakinin (Pea-SK-I).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
OC Blattidae; Periplaneta.
OC NCBI_TaxID=6978;
RN [1]
RP SEQUENCE.
RX TISSUE=Corpora cardiaca;
MEDLINE=90137180; PubMed=2615921;
RA Veenstra J.A.;
RT "Isolation and structure of two gastrin/CK-like neuropeptides from
RT the American cockroach homologous to the leucosulfakinins."
RL Neuropeptides 14:145-149(1989).
CC -1- FUNCTION: Stimulates hindgut contractions.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR PIR; A06056; A06056.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Hormone; Amidation; Sulfation.
FT MOD RES 6
FT MOD RES 11
FT MOD RES 11
SQ SEQUENCE 11 AA; 1445 MW; 8B4E0680E86B5AAB CRC64;

Query Match
Best Local Similarity 27.0%; Score 17; DB 1; Length 11;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 4 ERFPD 8
Db 1 ERFDD 5

RESULT 29
ADFB_TENMO STANDARD; PRT; 13 AA.
ID ADFB_TENMO STANDARD; PRT; 13 AA.
AC P83109;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Antidiuretic factor B (ADFB).
OS Tenebrio molitor (Yellow mealworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformata;
OC Tenebrionidae; Tenebrio.
OC NCBI_TaxID=7067;
RN [1]
RP SEQUENCE, FUNCTION, TISSUE SPECIFICITY, MASS SPECTROMETRY, AND
RP SYNTHESIS.
RX TISSUE=Head;
RX MEDLINE=22465067; PubMed=12576082;
RA Eugemeier R.A., Wiehart U.M., Nicolson S.W., Schoofs L., Schegg K.M.,
RA Hull U.J., Schooley D.A.;
RT "Isolation, identification and localization of a second beetle
RT antidiuretic peptide."
RL Peptides 24:27-34(2003).
CC -1- FUNCTION: Inhibitor of fluid secretion by Malpighian tubules. Uses
CC cGMP as second messenger. May function as an antidiuretic
CC hormone.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Brain. Appears to be mainly expressed in two
CC pairs of bilaterally symmetrical cells in the protocerebrum.
CC -1- MASS SPECTROMETRY: MW=1560.33; METHOD=MALDI.
KW Neuropeptide; Hormone.
SQ SEQUENCE 13 AA; 1562 MW; 0240A45048BA632B CRC64;

Query Match
Best Local Similarity 27.0%; Score 17; DB 1; Length 13;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IYG 3
Db 10 IYG 12

RESULT 30
NSK2_SARBU STANDARD; PRT; 14 AA.
ID NSK2_SARBU STANDARD; PRT; 14 AA.
AC P41453;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Neosulfakinin-II (NEB-SK-II).
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OC NCBI_TaxID=7385;
RN [1]
RP SEQUENCE.
RX TISSUE=Head;
RX MEDLINE=93083101; PubMed=1360367;
RA Fongy A., Schoofs L., Proost P., van Damme J., de Loof A.;
RT "Isolation and primary structure of two sulfakinin-like peptides from
RT the fleshfly, Neobellieria bullata."
RL Comp. Biochem. Physiol. 103C:135-142(1992).
CC -1- FUNCTION: Myotonic peptide.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR PIR; A56632; A56632.
DR InterPro; IPR001651; Gastrin.

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DR PROSITE: P800259; GASTRIN; 1.  
 KM Neuropeptide; Amidation; Sulfation.  
 FT MOD RES 9 SUIFATON (POTENTIAL).  
 FT MOD RES 14 AMIDATION (POTENTIAL).  
 SQ SEQUENCE 14 AA; 1794 MW; 884E06D5B61C62AA CRC64;

Query Match  
 Best Local Similarity 27.0%; Score 17; DB 1; Length 14;  
 Best Local Similarity 60.0%; Pred. No. 3.6e+03;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPD 8  
 DB 4 EOFFD 8

RESULT 31  
 TKNL\_SCHGR STANDARD; PRT; 14 AA.  
 ID TKNL\_SCHGR  
 AC P82470;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Tachykinin-1 (Secg-midgut-TK).  
 OS Schistocerca gregaria (Desert locust).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;  
 OC Acridoidea; Acrididae; Cyrtacanthacridinae; Schistocerca.  
 OX NCBI\_TaxID=7010;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Midgut;  
 RX MEDLINE=20050081; PubMed=10581195;  
 RA Vealet D., Baggerman G., Dervu R., Maelkens E., Meusen T.,  
 RA Vander Water G., De Loof A., Schoofs L.;  
 RT "Identification of a new tachykinin from the midgut of the desert  
 locust, *Schistocerca gregaria*, by ESI-MS/MS mass spectrometry.";  
 RL Biochem. Biophys. Res. Commun. 265:237-242(1999).  
 CC -1- FUNCTION: Myoactive peptide. Increases the amplitude and frequency  
 of spontaneous contractions and tonus of hindgut muscle.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Midgut.  
 CC -1- MASS SPECTROMETRY: MW=1493.79; METHOD=Electrospray.  
 CC -1- SIMILARITY: SIMILAR TO THE COCKROACH LEPTIN 3, A TACHYKININ-  
 RELATED PEPTIDE ALSO CONFINED TO THE MIDGUT.  
 KM Tachykinin; Neuropeptide; Amidation.  
 FT MOD RES 14  
 SQ SEQUENCE 14 AA; 1496 MW; CA4C578C0169FC72 CRC64;

Query Match  
 Best Local Similarity 27.0%; Score 17; DB 1; Length 14;  
 Best Local Similarity 75.0%; Pred. No. 3.6e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGER 5  
 DB 11 YGTR 14

RESULT 32  
 UC04\_MAIZE STANDARD; PRT; 14 AA.  
 ID UC04\_MAIZE  
 AC P80610;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 128).  
 OS Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 OX NCBI\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE=Coleoptile;  
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,  
 RA Pernollet J.-C., Zivy M., de Vienne D.;  
 RT "The maize two dimensional gel protein database: towards an integrated  
 genome analysis program.";  
 RL Theor. Appl. Genet. 93:997-1005(1996).  
 CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
 protein is: 6.8, its MW is: 34.6 kDa.  
 DR Maize-2DPAGE; P80610; COLEOPTILE.  
 DR MaizeDB; 123926; ...  
 FT MOD TER 1  
 FT NON TER 1  
 SQ SEQUENCE 14 AA; 1393 MW; C1451BA116D4AD CRC64;

Query Match  
 Best Local Similarity 27.0%; Score 17; DB 1; Length 14;  
 Best Local Similarity 75.0%; Pred. No. 3.6e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 DENF 11  
 DB 2 DEGF 5

RESULT 33  
 AL11\_CYPDO STANDARD; PRT; 8 AA.  
 ID AL11\_CYPDO  
 AC P82152;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Cydia pomonella 1.  
 OS Cydia pomonella (Coddling moth).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Dirryata;  
 OC Tortricoidae; Tortricidae; Olethreutinae; Cydia.  
 OX NCBI\_TaxID=82600;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Larva;  
 RX MEDLINE=8054539; PubMed=9392829;  
 RA Duvé H., Johnson A.H., Maestro J.-L., Scott A.G., Winstanley D.,  
 RA Davey M., East P.D., Thope A.,  
 RT "Lepidopteran peptides of the allatostatin superfamily.";  
 RL Peptides 18:1301-1309(1997).  
 CC -1- SIMILARITY: Belongs to the allatostatin family.  
 KM Neuropeptide; Amidation.  
 FT MOD RES 8  
 SQ SEQUENCE 8 AA; 934 MW; C82879C45B51F775 CRC64;

Query Match  
 Best Local Similarity 25.4%; Score 16; DB 1; Length 8;  
 Best Local Similarity 60.0%; Pred. No. 1.4e+05;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 PDENF 11  
 DB 2 PHYNF 6

RESULT 34  
 FAR7\_ASCSU STANDARD; PRT; 8 AA.  
 ID FAR7\_ASCSU  
 AC P43171;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE FMRPamide-like neuropeptide Af7.  
 OS Ascaris suum (Pig roundworm) (Ascaris lumbricoidea).  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascarididae; Ascaridoidea;  
 OC Ascarididae; Ascaris.  
 OX NCBI\_TaxID=6253;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=95380362; PubMed=7651904;



```

RA Cowden C., Stretton A.O.W.;
RT "Eight novel FMRFamide-like neuropeptides isolated from the nematode
RL Ascaris suum.";
CC Peptides 16:491-500(1995).
CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
KW family.
KW Neuropeptide; Amidation.
FT MOD RES 8
SQ SEQUENCE 8 AA; 963 MW; 9CD40059DA17687D CRC64;

Query Match 25.4%; Score 16; DB 1; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GERP 6
DB 2 GPRF 5

RESULT 35
FAR1_CALVO STANDARD; PRT; 9 AA.
AC P41856;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRFamide 1.
OS Calliphora vomitoria (Blue blowfly).
CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
CC Calliphoridae; Calliphora.
NCBI_TaxID=27454;

SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=9219611; PubMed=1549595;
RA Duvé H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliFMRFamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -1- FUNCTION: Able to induce fluid secretion from the isolated
CC salivary gland of Calliphora.
CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
DR PIR; A41978; A41978.
KW Neuropeptide; Amidation.
FT MOD RES 9
SQ SEQUENCE 9 AA; 1169 MW; 29D00699CAB6C67 CRC64;

Query Match 25.4%; Score 16; DB 1; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 PDENP 11
DB 2 PQQDF 6

RESULT 36
FAR2_CALVO STANDARD; PRT; 9 AA.
AC P41857;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRFamide 2.
OS Calliphora vomitoria (Blue blowfly).
CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
CC Calliphoridae; Calliphora.
NCBI_TaxID=27454;

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RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=9219611; PubMed=1549595;
RA Duvé H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliFMRFamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -1- FUNCTION: Able to induce fluid secretion from the isolated
CC salivary gland of Calliphora.
CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
DR PIR; A41978; A41978.
KW Neuropeptide; Amidation.
FT MOD RES 9
SQ SEQUENCE 9 AA; 1114 MW; 2F0B0699CAB6C5A7 CRC64;

Query Match 25.4%; Score 16; DB 1; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 PDENP 11
DB 2 PQQDF 6

RESULT 37
FAR3_CALVO STANDARD; PRT; 9 AA.
AC P41858;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRFamide 3.
OS Calliphora vomitoria (Blue blowfly).
CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
CC Calliphoridae; Calliphora.
NCBI_TaxID=27454;

SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=9219611; PubMed=1549595;
RA Duvé H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliFMRFamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -1- FUNCTION: Able to induce fluid secretion from the isolated
CC salivary gland of Calliphora.
CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
DR PIR; A41978; A41978.
KW Neuropeptide; Amidation.
FT MOD RES 9
SQ SEQUENCE 9 AA; 1114 MW; 2F0B0699CAB6C5A7 CRC64;

Query Match 25.4%; Score 16; DB 1; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 PDENP 11
DB 2 PQQDF 6

RESULT 38
FRF1_SARBU STANDARD; PRT; 9 AA.
AC P83350;

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DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Neo-FMRamide 1.  
 OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 CC Sarcophagidae; Sarcophaga.  
 CC NCB1\_TaxID=7385;  
 RN [1]  
 RP SEQUENCE, AMIDATION, AND FUNCTION.  
 RC TISSUE=CNS;  
 RX MEDLINE=22342733; PubMed=12438685;  
 RA Meunier T., Mertens I., Clynen E., Baggerman G., Nichols R.,  
 RA Nachman R.J., Hybrechts R., De loof A., Schoofs L.,  
 RT "Identification in *Drosophila melanogaster* of the invertebrate G  
 RT protein-coupled FMRamide receptor".  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).  
 CC -1- FUNCTION: Has modulatory actions at skeletal neuromuscular  
 CC junctions.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)  
 CC family.  
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.  
 FT MOD RES 9 9 AMIDATION.  
 FT MOD RES 9 9 AMIDATION.  
 SQ SEQUENCE 9 AA; 1155 MW; 2D810699CAB6C5A7 CRC64;  
 Query Match 25.4%; Score 16; DB 1; Length 9;  
 Best Local Similarity 40.0%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 OY 7 PDENP 11  
 DB 2 PSODF 6  
 RESULT 39  
 TKC1\_CALVO STANDARD; PRT; 9 AA.  
 AC P41517;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Callitachykintin I.  
 OS Calliphora vomitoria (Blue blowfly).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 CC Calliphoridae; Calliphora.  
 CC NCB1\_TaxID=27454;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RX MEDLINE=95075727; PubMed=7984492;  
 RA Lundquist C.T., Cloutens F.L., Holman G.M., Nichols R., Nachman R.J.,  
 RA Naessel D.R.,  
 RT "Callitachykintin I and II, two novel myotropic peptides isolated from  
 RT the blowfly, *Calliphora vomitoria*, that have resemblances to  
 RT tachykintins".  
 RL Peptides 15:761-768(1994).  
 CC -1- FUNCTION: Myoactive peptide.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.  
 KW Tachykintin; Neuropeptide; Amidation.  
 FT MOD RES 9 9 AMIDATION.  
 SQ SEQUENCE 9 AA; 981 MW; 2417C86B59CD1B7 CRC64;  
 Query Match 25.4%; Score 16; DB 1; Length 9;  
 Best Local Similarity 75.0%; Pred. NO. 1.4e+05;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 2 YGER 5  
 DB 6 YGVR 9

RESULT 40  
 TKC1\_LOCMI STANDARD; PRT; 9 AA.  
 AC P16223;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Locustatachykintin I (TK-I).  
 OS Locusta migratoria (Migratory locust).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;  
 CC Acridoidea; Acrididae; Oedipodinae; Locusta.  
 CC NCB1\_TaxID=7004;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=90184489; PubMed=2211766;  
 RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de loof A.,  
 RT "Locustatachykintin I and II, two novel insect neuropeptides with  
 RT homology to peptides of the vertebrate tachykintin family".  
 RL FEBS Lett. 261:397-401(1990).  
 CC -1- FUNCTION: Myoactive peptide. Stimulates the contraction of the  
 CC oviduct and foregut.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.  
 DR PIR; S08265; ECLQ1M.  
 KW Tachykintin; Neuropeptide; Amidation.  
 FT MOD RES 9 9 AMIDATION.  
 FT MOD RES 9 9 AMIDATION.  
 SQ SEQUENCE 9 AA; 939 MW; 2389C86B59C865A7 CRC64;  
 Query Match 25.4%; Score 16; DB 1; Length 9;  
 Best Local Similarity 75.0%; Pred. NO. 1.4e+05;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 2 YGER 5  
 DB 6 YGVR 9  
 RESULT 41  
 PORB\_MERTM STANDARD; PRT; 10 AA.  
 AC P80901;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Pyruvate synthase subunit porb (EC 1.2.7.1) (Pyruvate oxidoreductase  
 DE beta chain) (POR) (Pyruvic-ferredoxin oxidoreductase beta subunit)  
 DE (Fragment).  
 GN PORB  
 OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).  
 CC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriales;  
 CC Methanobacteriaceae; Methanothermobacter.  
 CC NCB1\_TaxID=79529;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=97261844; PubMed=9108258;  
 RA Tersteegen A., Linder D., Thauer R.K., Hedderich R.,  
 RT "Structures and functions of four anaerobic 2-oxoacid oxidoreductases  
 RT in *Methanobacterium thermoautotrophicum*".  
 RL Eur. J. Biochem. 244:862-868(1997).  
 CC -1- CATALYTIC ACTIVITY: Pyruvate + CoA + oxidized ferredoxin = acetyl-  
 CC CoA + CO(2) + reduced ferredoxin.  
 CC -1- SUBUNIT: Heterotrimer of one alpha, one beta, one delta and one  
 CC gamma chain.  
 CC -1- MISCELLANEOUS: Has a pH optimum of 10.0 and an optimal temperature  
 CC of 80 degrees Celsius.  
 KW Oxidoreductase.  
 FT NON TER 10 10  
 FT NON TER 10 10  
 SQ SEQUENCE 10 AA; 1232 MW; 167011DAF6DB0760 CRC64;

Query Match 25.4%; Score 16; DB 1; Length 10;  
 Best Local Similarity 40.0%; Pred. No. 3.8e+03;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 PDENP 11  
 ||:|  
 DB 4 PEQXF 8

## RESULT 42

PPCK\_FASHE STANDARD; PRT; 10 AA.  
 ID PPCK\_FASHE STANDARD; PRT; 10 AA.  
 AC P80525;  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Putative phosphoenolpyruvate carboxylase [GTP] (EC 4.1.1.32)  
 DE (Phosphoenolpyruvate carboxylase) (PEPCK) (Newly excysted juvenile protein 1) (Fragment).  
 DE Fasciola hepatica (liver fluke).  
 OS Fasciola hepatica; Trematoda; Digenea;  
 OC Eukaryota; Metazoa; Platyhelminthes; Fasciolidae; Fasciola.  
 CC Echinostomida; Echinostomata; Fasciolidae; Fasciola.  
 OX NCBI\_TaxID=6192;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=95366993; PubMed=7639732;  
 RA Tkalcovic J., Ashman K., Meusen E.;  
 RT "Fasciola hepatica: rapid identification of newly excysted juvenile proteins";  
 RL Biochem. Biophys. Res. Commun. 213:169-174(1995).  
 CC -1- CATALYTIC ACTIVITY: GTP + oxaloacetate = GDP + phosphoenolpyruvate + CO(2).  
 CC -1- SIMILARITY: Belongs to the phosphoenolpyruvate carboxylase (GTP) family.  
 CC InterPro; IPR008209; PEP\_carboxykin.  
 DR PROSITE; PS00505; PEPCK\_GTP; PARTIAL.  
 KW Lyase; Decarboxylase; GTP-binding.  
 FT NON TER 10  
 SQ SEQUENCE 10 AA; 1069 MW; 8393A6187AA9C87A CRC64;

Query Match 25.4%; Score 16; DB 1; Length 10;  
 Best Local Similarity 66.7%; Pred. No. 3.8e+03;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPD 8  
 :||  
 DB 1 YPD 3

## RESULT 43

TKL2\_LOCOMI STANDARD; PRT; 10 AA.  
 ID TKL2\_LOCOMI STANDARD; PRT; 10 AA.  
 AC P16224;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Locustatachykinin II (TK-II).  
 OS Locusta migratoria (Migratory locust).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
 CC Acridoidea; Acrididae; Caelifera; Locusta.  
 OX NCBI\_TaxID=7004;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=90184489; PubMed=2311766;  
 RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;  
 RT "Locustatachykinin I and II: two novel insect neuropeptides with homology to peptides of the vertebrate tachykinin family";  
 RL FEBS Lett. 261:397-401(1990).  
 CC -1- FUNCTION: Myoactive peptide. Stimulates the contraction of the oviduct and foregut.  
 CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.  
 DR PIR; S08266; ECLQ2M.  
 KW Tachykinin; Neuropeptide; Amidation.  
 FT MOD RES 10  
 SQ SEQUENCE 10 AA; 1066 MW; 5D52CD6B59C865B7 CRC64;

Query Match 25.4%; Score 16; DB 1; Length 10;  
 Best Local Similarity 75.0%; Pred. No. 3.8e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGER 5  
 |||  
 DB 7 YGVR 10

## RESULT 44

TKL3\_LOCOMI STANDARD; PRT; 10 AA.  
 ID TKL3\_LOCOMI STANDARD; PRT; 10 AA.  
 AC P30249;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Locustatachykinin III (TK-III).  
 OS Locusta migratoria (Migratory locust).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
 CC Acridoidea; Acrididae; Caelifera; Locusta.  
 OX NCBI\_TaxID=7004;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=91219696; PubMed=212575;  
 RA Schoofs L., Holman G.M., Hayes T.K., Kochansky J.P., Nachman R.J., de Loof A.;  
 RT "Locustatachykinin III and IV: two additional insect neuropeptides with homology to peptides of the vertebrate tachykinin family";  
 RL Regul. Pept. 31:199-212(1990).  
 CC -1- FUNCTION: Myoactive peptide. Stimulates the contraction of the oviduct and foregut.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.  
 DR PIR; A60073; ECLQ3M.  
 KW Tachykinin; Neuropeptide; Amidation.  
 FT MOD RES 10  
 SQ SEQUENCE 10 AA; 1065 MW; C452CD6B59C87DC6 CRC64;

Query Match 25.4%; Score 16; DB 1; Length 10;  
 Best Local Similarity 75.0%; Pred. No. 3.8e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGER 5  
 |||  
 DB 7 YGVR 10

## RESULT 45

TKSL\_AEDAE STANDARD; PRT; 10 AA.  
 ID TKSL\_AEDAE STANDARD; PRT; 10 AA.  
 AC P42634;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Stalokinin I.  
 OS Aedes aegypti (Yellowfever mosquito).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Aedes.  
 OX NCBI\_TaxID=7159;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=94105119; PubMed=8278354;  
 RA Champagne D.E., Ribeiro J.W.C.;  
 RT "Stalokinin I and II: vasodilatory tachykinins from the yellow fever

RT mosquito Aedes aegypti";  
 RU Proc Natl Acad Sci U.S.A. 91:139-142(1994).  
 CC -1- FUNCTION: Vasodilatory peptide. May activate macrophages at the  
 CC site of feeding.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR: A49581; A49581.  
 DR InterPro: IPR002040; Tachy Neurokinin.  
 DR PROSITE: PS00267; TACHYKININ; 1.  
 KM Tachykinin; Neuropeptide; Amidation.  
 FT MOD\_RES 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1145 MW; 3DCFD6B59C33AA8 CRC64;

Query Match 25.4%; Score 16; DB 1; Length 10;  
 Best Local Similarity 50.0%; Pred. No. 3.8e+03;  
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 GERP 6  
 DB 3 GDKF 6

Search completed: August 30, 2004, 10:50:22  
 Job time : 2.89527 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:41:54 ; Search time 3.30743 Seconds  
(without alignments)  
319.918 Million cell updates/sec

Title: US-09-720-469A-6  
Perfect score: 63  
Sequence: 1 IYGERPPDENF 11

Scoring table: BLASTSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 1638

Minimum DB seq length: 8  
Maximum DB seq length: 14

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	39.7	10	2	A60476	S-layer protein -
2	38.1	9	2	PT0315	Ig heavy chain CRD
3	36.5	12	2	S26556	T-cell receptor be
4	36.5	12	2	PA0047	Protein QAI00045 -
5	36.5	11	2	E60409	Substance P-like p
6	31.7	9	2	PT0324	Ig heavy chain CRD
7	31.7	13	2	S29488	GTP-binding protei
8	31.7	14	2	A42473	emk leader peptid
9	30.2	8	2	A46306	spasmogenic toxin
10	30.2	10	2	B56899	serum heterodimer,
11	30.2	12	2	S26554	T-cell receptor be
12	30.2	13	2	S47362	Ig heavy chain rec
13	28.6	8	2	PH1407	T-cell antigen rec
14	28.6	9	2	S10784	enamelin 1 - bovin
15	28.6	10	2	B33710	ornithine decarbox
16	28.6	10	2	A33143	pneumadin - rat
17	28.6	11	2	B60409	kaesin-like pept
18	28.6	11	2	C60409	kaesin-like pept
19	28.6	11	2	S07203	upercleln - frog
20	28.6	12	2	S26552	T-cell receptor be
21	28.6	12	2	P00730	unidentified 5.4/3
22	28.6	13	2	S32473	lymnaadPamide 3 - 9
23	28.6	14	2	G44957	photosystem II oxy
24	28.6	14	2	A54370	inorganic diphosph
25	27.0	9	2	G68502	kidney and bladder
26	27.0	9	2	D41978	callitricamide 4 -
27	27.0	9	2	S36850	Ig heavy chain V r
28	27.0	9	2	I49406	bone gla protein -
29	27.0	10	2	PQ0753	beta-fructofuranos

30	17	27.0	10	2	A61354	Carnitine medium/1
31	17	27.0	11	1	GMR0L	leucosulfakinin -
32	17	27.0	11	2	A58502	38K kidney stone p
33	17	27.0	11	2	JQ2307	hypothetical 1.5K
34	17	27.0	11	2	A60656	perisulfakinin - A
35	17	27.0	11	2	S23926	major glycoprotein
36	17	27.0	12	2	PH1462	T-cell receptor be
37	17	27.0	13	2	A32734	enkephalin precurs
38	17	27.0	14	2	A56632	neosulfakinin-II -
39	17	27.0	14	2	PH1356	Ig heavy chain DJ
40	17	27.0	14	2	A59018	MUC1 enhancer bind
41	16.5	26.2	12	2	S15815	translacion elonga
42	16	25.4	8	2	S11078	glucose-6-phosphat
43	16	25.4	9	2	PT0653	T-cell receptor be
44	16	25.4	8	2	A61230	caldesmestrin, car
45	16	25.4	9	2	D57444	neuropeptide Grp-A

## ALIGNMENTS

```
RESULT 1
A:Accession: A60476
S:Layer protein - Bacillus thuringiensis (fragment)
C:Species: Bacillus thuringiensis
C>Date: 20-Feb-1993 #sequence_revision 20-Feb-1993 #text_change 12-Mar-1993
R:Accession: A60476
R:Location: M.D.; Beverage, T.J.
J: Bacteriol. 171, 6656-6667, 1989
A:Title: Characterization of a dynamic S layer on Bacillus thuringiensis.
A:Reference number: A60476; PMID:90078111; PMID:2592346
A:Molecule type: protein
A:Residues: 110 <LUC>
C:Comment: The S-layer, or surface array, is the outermost component of several archaea

Query Match          39.7%; Score 25; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GERFPD 8
DB 2 GKTFPD 7

RESULT 2
PT0315
I: Ig heavy chain CRD3 region (clone 6-109) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0315
R:Yamada, M.; Maeserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J: Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j
A:Reference number: PT0222; PMID:91108357; PMID:1899102
A:Molecule type: DNA
A:Residues: 1-9 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match          38.1%; Score 24; DB 2; Length 9;
Best Local Similarity 55.6%; Pred. No. 2.8e+05;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 GERPPDENF 11
DB 1 GERFLSF 9

RESULT 3
S26556
T-cell receptor beta chain (clone Cw3/2C3) - mouse (fragment)
```

C:Species: Mus musculus (house mouse)  
 C:Date: 13-Jan-1995 #sequence\_revision 17-Apr-1998 #text\_change 17-Mar-1999  
 C:Accession: S26556  
 R:Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid  
 J. Exp. Med. 176, 439-447, 1992  
 A:Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor  
 A:Reference number: S26552; PMID:92364546; PMID:1380061  
 A:Accession: S26556  
 A:Molecule type: mRNA  
 A:Residues: 1-12 <C>AS>  
 A:Cross-references: EMBL:X58006  
 A:Experimental source: cytolitic T-lymphocyte, clone CW3/2C3  
 A:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: T-cell receptor

Query Match 36.5%; Score 23; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGER 5  
 |||  
 |||  
 Db 5 YGER 8

## RESULT 4

Protein QAI00045 - Arabidopsis thaliana (fragment)  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 06-Jun-1997  
 C:Accession: P40047  
 R:Kano, M.; Kawakami, T.; Miyake, N.; Tsugita, A.  
 submitted to JIPD, July 1994  
 A:Description: Separation and characterization of Arabidopsis proteins by two-dimensional  
 A:Reference number: P40001  
 A:Accession: P40047  
 A:Molecule type: protein  
 A:Residues: 1-12 <K>AM>

Query Match 36.5%; Score 23; DB 2; Length 12;  
 Best Local Similarity 50.0%; Pred. No. 4.4e+02;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 GERPD 8  
 |||  
 |||  
 Db 5 GDXLPD 10

## RESULT 5

substance P-like peptide I - frog (Pseudophryne guentheri)  
 C:Species: Pseudophryne guentheri  
 C:Date: 30-Jan-1993 #sequence\_revision 30-Jan-1993 #text\_change 02-Sep-2000  
 C:Accession: E60409  
 R:Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossea, F.; Roberts, J.D.; Melchior  
 Peptides 11, 299-304, 1990  
 A:Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austro  
 A:Reference number: A60409; PMID:90287814; PMID:2356157  
 A:Accession: E60409  
 A:Molecule type: protein  
 A:Residues: 1-11 <S>IM>  
 C:Superfamily: unassigned animal peptides  
 C:Keywords: amidated carboxyl end; pyroglutamic acid  
 P11/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental  
 P11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 33.3%; Score 21; DB 2; Length 11;  
 Best Local Similarity 80.0%; Pred. No. 9.3e+02;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 PDENF 11  
 |||  
 |||  
 Db 4 PDEFF 8

## RESULT 6

PT0324  
 Ig heavy chain CRD3 region (clone 02-106C) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
 C:Accession: PT0324  
 R:Yamada, M.; Masserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
 J. Exp. Med. 173, 395-407, 1991  
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and jc  
 A:Reference number: PT0222; PMID:91108337; PMID:1899102  
 A:Accession: PT0324  
 A:Molecule type: DNA  
 A:Residues: 1-9 <Y>AM>  
 A:Experimental source: B lymphocyte  
 C:Keywords: heterotetramer; immunoglobulin

Query Match 31.7%; Score 20; DB 2; Length 9;  
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGERF 6  
 |||  
 |||  
 Db 4 YGESY 8

## RESULT 7

S29488  
 GTP-binding protein o-rab3 - marbled electric ray (fragment)  
 C:Species: Torpedo marmorata (marbled electric ray)  
 C:Date: 22-Nov-1993 #sequence\_revision 27-Feb-1997 #text\_change 13-Mar-1997  
 C:Accession: S29488  
 R:Polymardt, W.; Pevsner, J.; Elferink, L.A.; Scheller, R.H.  
 FEBS Lett. 317, 53-56, 1993  
 A:Title: Association of three small GTP-binding proteins with cholinergic synaptic vesicle  
 A:Reference number: S29485; PMID:93154521; PMID:8428634  
 A:Accession: S29488  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-13 <Y>OL>

Query Match 31.7%; Score 20; DB 2; Length 13;  
 Best Local Similarity 75.0%; Pred. No. 1.7e+03;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 DENF 11  
 |||  
 |||  
 Db 5 DQNP 8

## RESULT 8

A42473  
 ermK leader peptide - Bacillus licheniformis  
 C:Species: Bacillus licheniformis  
 C:Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 24-Sep-1999  
 C:Accession: A42473; I39884  
 R:Kwak, J.H.; Choi, E.C.; Weisblum, B.  
 J. Bacteriol. 173, 4725-4735, 1991  
 A:Title: Transcriptional attenuation control of ermK, a macrolide-lincosamide-streptogramin  
 A:Reference number: A42473; PMID:91310580; PMID:1713206  
 A:Accession: A42473  
 A:Molecule type: DNA  
 A:Residues: 1-14 <R>MA>  
 R:Gryczan, T.; Israeli-Reches, M.; Del Bue, M.; Dubnau, D.A.  
 Mol. Gen. Genet. 194, 349-356, 1994  
 A:Title: DNA sequence and regulation of ermM, a macrolide-lincosamide-streptogramin B res  
 A:Reference number: I39884; PMID:84245158; PMID:6429477  
 A:Accession: I39884  
 A:Status: preliminary; translated from GB/EMBL/DBU  
 A:Molecule type: DNA  
 A:Residues: 1-14 <R>ES>  
 A:Cross-references: GB:M29832; NID:G143199; PIDN:AAA22598.1; PID:G143200  
 C:Superfamily: unassigned leader peptides

Query Match 31.7%; Score 20; DB 2; Length 14;  
 Best Local Similarity 66.7%; Pred. No. 1.9e+03;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 RFPDEN 10  
 DB 8 RFPDEN 13

## RESULT 9

A46306  
 spasmogenic toxin PNV1 - spider (Phonetreria nigriventer) (fragment)

C/Species: Phonetreria nigriventer  
 C/Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 17-Mar-1999  
 C/Accession: A46306  
 R/Marangoni, S.; Borges, N.C.C.; Marangoni, R.A.; Antunes, E.; Vieira, C.A.; Novello, J.  
 Toxicol 31, 377-384, 1993  
 A/Title: Biochemical characterization of a vascular smooth muscle contracting polypeptide  
 A/Reference number: A46306; MUID:93276438; PMID:8503129  
 A/Accession: A46306  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-8 <MAR>

Query Match 30.2%; Score 19; DB 2; Length 8;  
 Best Local Similarity 42.9%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 ERFPDEN 10  
 DB 1 EAFPGQS 7

## RESULT 10

B56899  
 serum heterodimer, 24K chain - sandbar shark (fragment)

C/Species: Carcharhinus plumbeus (sandbar shark)  
 C/Date: 11-Aug-1995 #sequence\_revision 11-Aug-1995 #text\_change 20-Jun-2000  
 C/Accession: B56899  
 R/Vazquez-Moreno, L.; Porath, J.; Schluter, S.F.; Marchalonis, J.J.  
 Comp. Biochem. Physiol. B 103, 563-568, 1992  
 A/Title: Purification of a novel heterodimer from shark (Carcharhinus plumbeus) serum by  
 A/Reference number: A56899; MUID:93025932; PMID:1458832  
 A/Accession: B56899  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-10 <VAR>  
 C/Keywords: glycoprotein; plasma

Query Match 30.2%; Score 19; DB 2; Length 10;  
 Best Local Similarity 57.1%; Pred. No. 2e+03;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 GERFPDE 9  
 DB 4 GERVNE 10

## RESULT 11

S26554  
 T-cell receptor beta chain (clone CW3/Cas7) - mouse (fragment)

C/Species: Mus musculus (house mouse)  
 C/Date: 13-Jan-1995 #sequence\_revision 17-Apr-1998 #text\_change 17-Mar-1999  
 C/Accession: S26554  
 R/Casanova, J.L.; Cerottini, J.C.; Mathes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid  
 J. Exp. Med. 176, 439-447, 1992  
 A/Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor  
 A/Reference number: S26554; MUID:92364546; PMID:1380061  
 A/Accession: S26554  
 A/Molecule type: mRNA  
 A/Residues: 1-12 <CAS>  
 A/Cross-references: EMBL:X68004

A/Experimental source: cytolytic T-lymphocyte, clone CW3/Cas7  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: T-cell receptor

Query Match 30.2%; Score 19; DB 2; Length 12;  
 Best Local Similarity 75.0%; Pred. No. 2.4e+03;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGER 5  
 DB 5 FGER 8

## RESULT 12

S47362  
 T-cell antigen receptor VJ junction beta chain - human

C/Species: Homo sapiens (man)  
 C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 05-Nov-1999  
 C/Accession: S47362  
 R/Lehner, P.J.  
 submitted to the EMBL Data Library, August 1994  
 A/Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T ce  
 A/Reference number: S47355  
 A/Accession: S47362  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-13 <LEH>  
 A/Cross-references: EMBL:E35688; NID:9527465; PIDN:CA84757.1; PID:9527466  
 C/Keywords: T-cell receptor

Query Match 30.2%; Score 19; DB 2; Length 13;  
 Best Local Similarity 60.0%; Pred. No. 2.6e+03;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGERF 6  
 DB 8 YNEGF 12

## RESULT 13

PH1407  
 Ig heavy chain V region (clone micro m+ 46-6 PCR) - mouse (fragment)

C/Species: Mus musculus (house mouse)  
 C/Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 17-Mar-1999  
 C/Accession: PH1407  
 R/Shirasawa, T.; Miyazoe, I.; Hagiwara, S.; Kimoto, H.; Shigemoto, K.; Taniguchi, M.; Ta  
 J. Exp. Med. 176, 1209-1214, 1992  
 A/Title: Heavy chain variable (VH) region diversity generated by VH gene replacement in t  
 la virus.  
 A/Reference number: PH1403; MUID:93018837; PMID:1402663  
 A/Accession: PH1407  
 A/Molecule type: DNA  
 A/Residues: 1-8 <SHI>  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin

Query Match 28.6%; Score 18; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RFP 7  
 DB 6 RFP 8

## RESULT 14

S10784  
 enamelrin i - bovine (fragment)

C/Species: Bos primigenius taurus (cattle)  
 C/Date: 19-Mar-1997 #sequence\_revision 21-Nov-1998 #text\_change 21-Nov-1998  
 C/Accession: S10784  
 R/Strawich, E.; Glimcher, M.J.  
 Eur. J. Biochem. 191, 47-56, 1990

A>Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is abdu  
A/Reference number: S10780; MUID:90336641; PMID:2379503  
A/Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austral  
A/Reference number: A60409; MUID:90287814; PMID:2356157  
A/Molecule type: protein  
A/Residues: 1-9 <STR>  
C/Keywords: enamel; phosphoprotein

Query Match 28.6%; Score 18; DB 2; Length 9;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 6 PPDENP 11  
DB 1 FPDYGF 6

## RESULT 15

B33710  
ornithine decarboxylase leader peptide - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 27-Feb-1990 #sequence\_revision 27-Feb-1990 #text\_change 24-Sep-1999

C/Accession: B33710

R;Men, L.; Huang, J.K.; Blackhear, P.J.

J. Biol. Chem. 264, 9016-9021, 1989

A/Title: Rat ornithine decarboxylase gene. Nucleotide sequence, potential regulatory ele

A/Reference number: A33710; MUID:89255378; PMID:2722815

A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra

A/Accession: B33710

A/Molecule type: mRNA

A/Residues: 1-10 <MEN>

A/Cross-references: GB:J04791; NID:9205807; PIDN:AAA6163.1; PID:9806309

C/Superfamily: unassigned leader peptides

Query Match 28.6%; Score 18; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 RFP 7  
DB 6 RFP 8

## RESULT 16

A33143  
pneumadin - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 16-Nov-1990 #sequence\_revision 16-Nov-1990 #text\_change 18-Aug-2000

C/Accession: A33143

R;Batra, V.K.; Mathur, M.; Mir, S.A.; Kapoor, R.; Kumar, M.A.

Regul. Pept. 30, 77-87, 1990

A/Title: Pneumadin: a new lung peptide which triggers antidiuresis.

A/Reference number: A33143; MUID:9110910; PMID:2274681

A/Accession: A33143

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-10 <BAT>

C/Superfamily: unassigned animal peptides

Query Match 28.6%; Score 18; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 YGE 4  
DB 1 YGE 3

## RESULT 17

B60409  
kassinin-like peptide K-I - frog (Pseudophryne guentheri)

C/Species: Pseudophryne guentheri

C/Date: 30-Jan-1993 #sequence\_revision 30-Jan-1993 #text\_change 18-Aug-2000

C/Accession: B60409

R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior

Peptides 11, 299-304, 1990

A/Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austral

A/Reference number: A60409; MUID:90287814; PMID:2356157

A/Accession: B60409

A/Molecule type: protein

A/Residues: 1-11 <SIM>

A/Note: this peptide was also found in a deamidated form

C/Superfamily: unassigned animal peptides

C/Keywords: amidated carboxyl end; pyroglutamic acid

F.11/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F.11/Modified site: amidated carboxyl end (Met) (partial) #status experimental

Query Match 28.6%; Score 18; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 PDE 9  
DB 4 PDE 6

RESULT 18  
C60409  
kassinin-like peptide K-II - frog (Pseudophryne guentheri)

C/Species: Pseudophryne guentheri

C/Date: 30-Jan-1993 #sequence\_revision 30-Jan-1993 #text\_change 18-Aug-2000

C/Accession: C60409

R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior

Peptides 11, 299-304, 1990

A/Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austral

A/Reference number: A60409; MUID:90287814; PMID:2356157

A/Accession: C60409

A/Molecule type: protein

A/Residues: 1-11 <SIM>

A/Note: this peptide was also found in a deamidated form

C/Superfamily: unassigned animal peptides

C/Keywords: amidated carboxyl end; pyroglutamic acid

F.11/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F.11/Modified site: amidated carboxyl end (Met) (partial) #status experimental

Query Match 28.6%; Score 18; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 PDE 9  
DB 4 PDE 6

RESULT 19  
S07203  
uperolein - frog (Uperoleia marmorata)

C/Species: Uperoleia marmorata

C/Date: 12-Feb-1993 #sequence\_revision 12-Mar-1993 #text\_change 18-Aug-2000

C/Accession: S07203

R;Anastasi, A.; Erspamer, V.; Endean, R.

Experientia 31, 394-395, 1975

A/Title: Structure of uperolein, a physalaemin-like endecapeptide occurring in the skin

A/Reference number: S07203; MUID:75131227; PMID:1120493

A/Accession: S07203

A/Molecule type: protein

A/Residues: 1-11 <ANR>

C/Superfamily: unassigned animal peptides

C/Keywords: amidated carboxyl end; pyroglutamic acid; skin; tachykinin

F.11/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F.11/Modified site: amidated carboxyl end (Met) #status experimental



Db 2 PDBN 5

## RESULT 20

S26552  
T-cell receptor beta chain (clone Cw3/701.1) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 13-Jan-1995 #sequence\_revision 17-Apr-1998 #text\_change 17-Mar-1999  
C/Accession: S26552  
R/Csanova, J.L.; Cecotini, J.C.; Matthes, M.; Necker, A.; Gounier, H.; Barra, C.; Wid  
J., Exp. Med. 176, 439-447, 1992  
A/Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor  
A/Reference number: S26512; MUID:92364546; PMID:1380061  
A/Accession: S26552  
A/Molecule type: mRNA  
A/Residues: 1-12 <CMS>  
A/Cross-references: EMBL:X68002  
A/Experimental source: cytolytic T-lymphocyte, clone Cw3/701.1  
C/Superfamily: Immunoglobulin V region; Immunoglobulin homology  
C/Keywords: T-cell receptor

Query Match 28.6%; Score 18; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 YGE 4  
|||  
Db 5 YGE 7

## RESULT 21

PQ0730  
unidentified 5.4/35k protein [imported] - rice (fragment)  
C/Species: Oryza sativa (rice)  
C/Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
C/Accession: PQ0730  
R/Komatsu, S.; Kajiwara, H.; Hirano, H.  
Theor. Appl. Genet. 86, 935-942, 1993  
A/Title: A rice protein library: a data-file of rice proteins separated by two-dimension  
A/Reference number: PQ0696  
A/Accession: PQ0730  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-12 <KOM>

Query Match 28.6%; Score 18; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 YGE 4  
|||  
Db 8 YGE 10

## RESULT 22

S32473  
LymnaeaFamide 3 - great pond snail  
C/Species: Lymnaea stagnalis (great pond snail)  
C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 20-Aug-1999  
C/Accession: S32473  
R/Johnson, A.H.; Rehfeld, J.F.  
Eur. J. Biochem. 213, 875-879, 1993  
A/Title: Lymnaeafamides, a new family of neuropeptides from the pond snail, Lymnaea stagnalis  
A/Reference number: S32471; MUID:93238777; PMID:8477756  
A/Accession: S32473  
A/Molecule type: protein  
A/Residues: 1-13 <JOH>  
A/Cross-references: PIDN:AAB26364.1; PID:G299631  
A/Experimental source: ganglia  
C/Keywords: amidated carboxyl end; neuropeptide  
F.13/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 28.6%; Score 18; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 4e+03;  
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 IYGERFPD 8  
|||  
Db 5 ISGSAFSD 12

## RESULT 23

G44957  
photosystem II oxygen-evolving complex protein 2 - common tobacco (cv. Samsun NN) (fragment)  
C/Species: Nicotiana tabacum (common tobacco)  
C/Date: 03-Jun-1993 #sequence\_revision 03-Jun-1993 #text\_change 18-Jun-1993  
C/Accession: G44957  
R/Takeda, S.; Sato, F.; Ida, K.; Yamada, Y.  
Plant Cell Physiol. 31, 215-221, 1990  
A/Title: Characterization of polypeptides that accumulate in cultured Nicotiana tabacum  
A/Reference number: A44957  
A/Accession: G44957  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-14 <TAK>

Query Match 28.6%; Score 18; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 4.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 YGE 4  
|||  
Db 2 YGE 4

## RESULT 24

A54370  
inorganic diphosphatase (EC 3.6.1.1) - cucurbit (fragment)  
C/Species: Cucurbita sp. (cucurbit)  
C/Date: 07-Jul-1995 #sequence\_revision 07-Jul-1995 #text\_change 03-Jun-2002  
C/Accession: A54370  
R/Sato, M.H.; Kasahara, M.; Ishii, N.; Homareda, H.; Matsui, H.; Yoshida, M.  
J. Biol. Chem. 269, 6725-6728, 1994  
A/Title: Purified vacuolar inorganic pyrophosphatase consisting of a 75-kDa polypeptide  
A/Reference number: A54370; MUID:94165068; PMID:8120031  
A/Accession: A54370  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-14 <SAT>  
C/Keywords: hydrolase

Query Match 28.6%; Score 18; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 4.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 PDE 9  
|||  
Db 11 PDE 13

## RESULT 25

G58502  
kidney and bladder stone protein - unidentified bacterium (fragment)  
C/Species: unidentified bacterium  
C/Date: 07-Feb-1997 #sequence\_revision 07-Feb-1997 #text\_change 10-Jul-1998  
C/Accession: G58502  
R/Binette, J.P.; Binette, M.B.  
submitted to the Protein Sequence Database, October 1996  
A/Description: The proteins of kidney and gallbladder stones.  
A/Reference number: A58501  
A/Accession: G58502  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-9 <BIN>  
A/Experimental source: human kidney stone, bladder stone

A>Note: a secondary sequence AAKENPXD was also found

Query Match 27.0%; Score 17; DB 2; Length 9;  
Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 PDENP 11  
|||  
Db 3 PDVXP 7

## RESULT 26

D41978  
Calliphora vomitoria  
C/Species: Calliphora vomitoria  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 17-Mar-1999  
C/Accession: D41978  
R/DuVe, H.; Johnson, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorpe  
Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992  
A/Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (desi  
A/Reference number: A41978; MUID:92196111; PMID:1549595  
A/Accession: D41978  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-9 <DUV>  
C/Keywords: amidated carboxyl end; neuropeptide

F,9/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 27.0%; Score 17; DB 2; Length 9;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 7 PDENP 11  
|||  
Db 2 PNQDF 6

## RESULT 27

S36850  
Ig heavy chain V region - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 06-Jan-1994 #sequence\_revision 01-Dec-1995 #text\_change 05-Nov-1999  
C/Accession: S36850  
R/Jacob, J.; Kelsce, G.  
Submitted to the EMBL Data Library, July 1992  
A/Description: In situ studies on the primary immune response to (4-hydroxy-3-nitropheny  
A/Reference number: S25024  
A/Accession: S36850  
A/Status: preliminary  
A/Molecule type: nucleic acid  
A/Residues: 1-9 <UAC>  
A/Cross-references: EMBL:X67387; NID:G50113; PID:G51594; PID:G1333871  
C/Keywords: heterotrimer; immunoglobulin

Query Match 27.0%; Score 17; DB 2; Length 9;  
Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 YGERP 6  
|||  
Db 5 YGSYP 9

## RESULT 28

I49406  
bone gla protein - western wild mouse (fragment)  
C/Species: Mus spretus (western wild mouse)  
C/Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999  
C/Accession: I49406  
R/Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H.  
Mamm. Genome 5, 349-355, 1994  
A/Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.  
A/Reference number: I49334; MUID:94319082; PMID:8043949

A/Accession: I49406  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-9 <RES>  
A/Cross-references: EMBL:U05695; NID:9497015; PIN:AA60465.1; PID:9642828

Query Match 27.0%; Score 17; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IYG 3  
|||  
Db 4 IYG 6

## RESULT 29

P00753  
beta-fructofuranosidase (EC 3.2.1.26) IIB - barley (fragment)  
C/Species: Hordeum vulgare (barley)  
C/Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 23-Mar-1995  
C/Accession: P00753  
R/Oberland, D.M.; Simmen, U.; Boller, T.; Wilmken, A.  
Plant Physiol. 101, 1331-1339, 1993  
A/Title: Purification and characterization of three soluble invertases from barley (Horde  
A/Reference number: P00752; MUID:94143483; PMID:8310063  
A/Accession: P00753  
A/Molecule type: protein  
A/Residues: 1-10 <OBE>  
A/Experimental source: leaf, cv. Express  
C/Keywords: alternative initiators; glycoprotein; glycosidase; hydrolase

Query Match 27.0%; Score 17; DB 2; Length 10;  
Best Local Similarity 60.0%; Pred. No. 4.6e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 PPDEN 10  
|||  
Db 2 PPDWN 6

## RESULT 30

A61354  
carnitine medium/long chain acyltransferase (EC 2.3.1.-) - rat (fragment)  
N/Alternate names: endoplasmic reticulum protein Exp61; glucose regulated protein GRP58;  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-May-1999  
C/Accession: A61354  
R/Murthy, M.S.R.; Pandey, S.V.  
Mol. Cell. Biochem. 122, 133-138, 1993  
A/Title: Carnitine medium/long chain acyltransferase of microsomes seems to be the previc  
A/Reference number: A61354; MUID:94049728; PMID:8232244  
A/Accession: A61354  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-10 <MUR>  
C/Keywords: acyltransferase

Query Match 27.0%; Score 17; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 DEN 10  
|||  
Db 8 DEN 10

## RESULT 31

GKROL  
leucosulfakinin - Madeira cockroach  
N/Alternate names: LSK  
C/Species: Leucophaea maderae (Madeira cockroach)  
C/Date: 17-Mar-1987 #sequence\_revision 17-Mar-1987 #text\_change 13-Sep-1996  
C/Accession: A01622

R;Nachman, R.J.; Holman, G.M.; Haddon, W.F.; Ling, N.

Science 234, 71-73, 1986

A;Title: Leucosulfakinin, a sulfated insect neuropeptide with homology to gastrin and ch

A;Reference number: A01622; MUID:8631858; PMID:3749893

A;Accession: A01622

A;Molecule type: protein

A;Residues: 1-11 <NAC>

C;Superfamily: gastrin

C;Keywords: amidated carboxyl end; hormone; sulfoprotein

F;6/Binding site: sulfate (Tyr) (covalent) #status experimental

F;11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 27.0%; Score 17; DB 1; Length 11;

Best Local Similarity 60.0%; Pred. No. 5.1e+03;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPD 8

DB 1 EQFDD 5

#### RESULT 32

A58502

38K kidney stone protein - unidentified bacterium (fragment)

C;Species: unidentified bacterium

C;Date: 07-Feb-1997 #sequence\_revision 07-Feb-1997 #text\_change 10-Jul-1998

C;Accession: A58502

R;Binette, J.P.; Binette, M.B.

submitted to the Protein Sequence Database, October 1996

A;Description: The proteins of kidney and gallbladder stones.

A;Reference number: A58501

A;Accession: A58502

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <BIN>

A;Experimental source: human kidney stone containing Ca ox.mono and dihyd, 1% struvite,

Query Match 27.0%; Score 17; DB 2; Length 11;

Best Local Similarity 60.0%; Pred. No. 5.1e+03;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GERFP 7

DB 7 GAXFP 11

#### RESULT 33

JQ2307

hypothetical 1.5K protein - tomato chloroplast (strain Toko)

C;Species: chloroplast lycopersicon esculentum (tomato)

C;Date: 10-Mar-1994 #sequence\_revision 28-Oct-1994 #text\_change 23-Mar-1995

C;Accession: JQ2307

R;Kawagoe, Y.; Kikuta, Y.

Theor. Appl. Genet. 81, 13-20, 1991

A;Title: Chloroplast DNA evolution in potato (Solanum tuberosum L.).

A;Reference number: JQ2306

A;Accession: JQ2307

A;Molecule type: DNA

A;Residues: 1-11 <KAW>

A;Experimental source: strain Toko

C;Genetics:

A;genome: chloroplast

C;Keywords: chloroplast

Query Match 27.0%; Score 17; DB 2; Length 11;

Best Local Similarity 60.0%; Pred. No. 5.1e+03;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 YGERP 6

DB 4 YDEEF 8

#### RESULT 34

A60656

perisulfakinin - American cockroach

C;Species: Periplaneta americana (American cockroach)

C;Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 11-Jul-1997

C;Accession: A60656

R;Venestra, J.A.

Neuropeptides 14, 145-149, 1989

A;Title: Isolation and structure of two gastrin/CKK-like neuropeptides from the American

A;Reference number: A60656; MUID:90137190; PMID:2615921

A;Accession: A60656

A;Molecule type: protein

A;Residues: 1-11 <VEE>

C;Comment: This neuropeptide stimulates hindgut contractions.

C;Keywords: amidated carboxyl end; neuropeptide; sulfoprotein

F;6/Binding site: sulfate (Tyr) (covalent) #status experimental

F;11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 27.0%; Score 17; DB 2; Length 11;

Best Local Similarity 60.0%; Pred. No. 5.1e+03;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPD 8

DB 1 EQFDD 5

#### RESULT 35

S23926

major glycoprotein PAS-6 - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 19-Mar-1997 #sequence\_revision 01-Feb-1999 #text\_change 01-Feb-1999

C;Accession: S23926

R;Kim, D.H.; Kanno, C.; Mizokami, Y.

Biochim. Biophys. Acta 1122, 203-211, 1992

A;Title: Purification and characterization of major glycoproteins, PAS-6 and PAS-7, from

A;Reference number: S23926; MUID:92353107; PMID:1643094

A;Accession: S23926

A;Molecule type: protein

A;Residues: 1-11 <KIM>

C;Keywords: glycoprotein; milk; blocked amino end

Query Match 27.0%; Score 17; DB 2; Length 11;

Best Local Similarity 42.9%; Pred. No. 5.1e+03;

Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 GERPDE 9

DB 3 GNNKPSE 9

#### RESULT 36

PH1462

T-cell receptor beta chain (clone A24/PEP1) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 11-Apr-1995

C;Accession: PH1462

R;Caanovva, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Ko

J. Exp. Med. 177, 811-820, 1993

A;Title: T cell receptor selection by and recognition of two class I major histocompatib

A;Reference number: PH1430; MUID:93171821; PMID:8436911

A;Accession: PH1462

A;Molecule type: mRNA

A;Residues: 1-12 <CAS>

A;Experimental source: cytoytic T-lymphocyte

C;Superfamily: immunoglobulin homology

C;Keywords: receptor; T-cell

Query Match 27.0%; Score 17; DB 2; Length 12;

Best Local Similarity 60.0%; Pred. No. 5.6e+03;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 PDENP 11

DB 7 PDYTF 11

## RESULT 37

A22734  
enkephalin precursor - sheep (fragment)  
C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C/Date: 20-Jul-1990 #sequence\_revision 20-Jul-1990 #text\_change 21-Jan-2000  
C/Accession: A32734  
R/Michanovic, R.; Ray, P.; Krugel, W.; Lewis, R.V.  
Biochem. Biophys. Res. Commun. 118, 299-303, 1984  
A/Title: Purification and sequence of an opioid peptide derived from ovine proenkephalin  
A/Reference number: A32734; MUID:84128045; PMID:6546517  
A/Accession: A32734  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-13 <MIC>  
C/Superfamily: proenkephalin  
C/Keywords: neuropeptide; opioid peptide

Query Match 27.0%; Score 17; DB 2; Length 13;  
Best Local Similarity 33.3%; Pred. No. 6.1e+03;  
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 IYGERF 6  
DB 4 VLGKRY 9

## RESULT 38

A56632  
neosulfakinin-II - flesh fly (Sarcophaga bullata)  
N/Alternate names: Neb-SK-II  
N/Contains: neosulfakinin-I (Neb-SK-I)  
C/Species: Sarcophaga bullata  
C/Date: 21-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 20-Jun-2000  
C/Accession: A56632  
R/Fonagy, A.; Schoofs, L.; Proost, P.; Van Damme, J.; De Loof, A.  
Comp. Biochem. Physiol. C 103, 135-142, 1992  
A/Title: Isolation and primary structure of two sulfakinin-like peptides from the flesh fly  
A/Reference number: A56632; MUID:93083101; PMID:1360367  
A/Accession: A56632  
A/Molecule type: protein  
A/Residues: 1-14 <FON>  
A/Experimental source: heads  
A/Note: sequence extracted from NCBI backbone (NCBIP:120391)  
C/Keywords: amidated carboxyl end; neuropeptide; sulfoprotein  
F/1-14/Product: neosulfakinin-II #status experimental <NSK2>  
F/6-14/Product: neosulfakinin-I #status experimental <NSK1>  
F/9/Binding site: sulfate (Tyr) (covalent) #status predicted  
F/14/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 27.0%; Score 17; DB 2; Length 14;  
Best Local Similarity 60.0%; Pred. No. 6.7e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 ERFPD 8  
DB 4 EQFPD 8

## RESULT 39

PH1356  
Ig heavy chain DJ region (clone C178-97) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C/Accession: PH1356  
R/Maserman, R.; Gallit, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
J. Exp. Med. 176, 1577-1581, 1992  
A/Title: Predominance of fetal type DJH joining in young children with B precursor lymph  
A/Reference number: PH1302; MUID:93094761; PMID:1460419  
A/Accession: PH1356

A/Molecule type: DNA  
A/Residues: 1-14 <MAS>  
C/Keywords: heterodimer; immunoglobulin

Query Match 27.0%; Score 17; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 6.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 IYG 3  
DB 4 IYG 6

## RESULT 40

A59018  
MUC1 enhancer binding protein 70K chain MUC1EBP-70 - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 08-May-1998  
C/Accession: A59018  
R/Abe, M.; Smith, C.J.; Larson, C.J.  
Submitted to the Protein Sequence Database, May 1998  
A/Description: Involvement of "Ku-like" proteins in the transcription of MUC1/DF3, a breast cancer cell line MCF-7  
A/Reference number: A59018  
A/Accession: A59018  
A/Molecule type: protein  
A/Residues: 1-14 <ABE>  
A/Experimental source: breast cancer cell line MCF-7  
A/Note: 3-Val was also found  
C/Keywords: DNA binding; heterodimer

Query Match 27.0%; Score 17; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 6.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 IYG 3  
DB 4 IYG 6

## RESULT 41

S15815  
translation elongation factor eEF-2 - rabbit (fragment)  
C/Species: Oryctolagus cuniculus (domestic rabbit)  
C/Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 18-Mar-1997  
C/Accession: S15815; S12970  
R/Price, N.T.; Redpath, N.T.; Severinov, K.V.; Campbell, D.G.; Russell, J.M.; Proud, C.G.  
FEBS Lett. 282, 253-258, 1991  
A/Title: Identification of the phosphorylation sites in elongation factor-2 from rabbit  
A/Reference number: S15815; MUID:91243806; PMID:2037042  
A/Accession: S15815  
A/Molecule type: protein  
A/Residues: 1-12 <OMP>  
R/Ovchinnikov, L.P.; Motuz, L.P.; Natapov, P.G.; Averbuch, L.J.; Wetrenhall, R.E.H.; Szyf  
FEBS Lett. 275, 209-212, 1990  
A/Title: Three phosphorylation sites in elongation factor 2.  
A/Reference number: S12970; MUID:91085562; PMID:2261989  
A/Accession: S12970  
A/Molecule type: protein  
A/Residues: 2-12 <OV>  
C/Superfamily: translation elongation factor 2; translation elongation factor Tu homology  
C/Keywords: GTP binding; phosphoprotein; protein biosynthesis  
F/8,10/Binding site: phosphate (Thr) (covalent) (by elongation factor 2 kinase) #status

Query Match 26.2%; Score 16.5; DB 2; Length 12;  
Best Local Similarity 71.4%; Pred. No. 7e+03;  
Matches 5; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 3 GE-RPFD 8  
DB 3 GETRFD 9

## RESULT 42

S11078  
 Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) - yeast (*Pichia jadinii*) (fragment)  
 C/Species: *Pichia jadinii*, *Candida utilis*  
 C/Date: 30-Jun-1991 #sequence\_revision 30-Sep-1991 #text\_change 05-Aug-1994  
 C/Accession: S11078  
 R/Eggestad, B.; Estonius, M.; Danielsson, O.; Persson, B.; Cederlund, E.; Kaiser, R.; Hol  
 FBS Lett. 269, 194-196, 1990  
 A/Title: Fast atom bombardment mass spectrometry and chemical analysis in determinations  
 A/Reference number: S11074; PMID:90353571; PMID:2387402  
 A/Accession: S11078  
 A/Molecule type: protein  
 A/Residues: 1-8 <EGE>  
 A/Note: the source is designated as *Pichia jadinii*  
 C/Keywords: acetylated amino end; oxidoreductase; pentose phosphate pathway  
 F/Modified site: acetylated amino end (Ser) #status experimental

Query Match 25.4%; Score 16; DB 2; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGER 5  
 DB 5 FGDR 8

RESULT 43  
 PT0653  
 T-cell receptor beta chain V-D-J region (121-3H) - mouse (fragment)  
 C/Species: *Mus musculus* (house mouse)  
 C/Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C/Accession: PT0653  
 R/Peeney, A.J.  
 J. Exp. Med. 174, 115-124, 1991  
 A/Title: Functional sequences of fetal T cell receptor beta chains have few N regions.  
 A/Reference number: PT0509; PMID:91277601; PMID:1711558  
 A/Accession: PT0653  
 A/Status: translation not shown  
 A/Molecule type: mRNA  
 A/Residues: 1-8 <FEE>  
 A/Experimental source: day 4 postnatal thymus, strain BALB/c  
 C/Keywords: T-cell receptor

Query Match 25.4%; Score 16; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GER 5  
 DB 6 GER 8

RESULT 44  
 A61230  
 calsequestrin, cardiac and slow skeletal muscle - northern leopard frog (fragment)  
 N/Alternate names: 58k dihydropyridine-binding protein; aspartactin; caltline; laminin-  
 C/Species: *Rana pipiens* (northern leopard frog)  
 C/Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 16-Jul-1999  
 C/Accession: A61230  
 R/McLeod, A.G.; Shen, A.C.Y.; Campbell, K.P.; Michalak, M.; Jorgensen, A.O.  
 Circ. Res. 69, 344-359, 1991  
 A/Title: Frog cardiac calsequestrin. Identification, characterization, and subcellular d  
 idium.  
 A/Reference number: A61230; PMID:91316784; PMID:1860177  
 A/Accession: A61230  
 A/Molecule type: protein  
 A/Residues: 1-9 <MCU>  
 C/Comment: Calsequestrin is a high-capacity and moderate-affinity calcium binding protei  
 C/Comment: Calsequestrin acts as a calcium buffer, and the release of calcium bound to d  
 C/Comment: The fast skeletal muscle isoform of calsequestrin can be phosphorylated in vi  
 C/Keywords: calcium binding; cardiac muscle; glycoprotein; heart; phosphoprotein; skelet

Query Match 25.4%; Score 16; DB 2; Length 9;

Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GERFP 7  
 DB 3 GLNFP 7

RESULT 45  
 D57444  
 neuropeptide Grp-AST B4 - two-spotted cricket  
 C/Species: *Gryllus bimaculatus* (two-spotted cricket)  
 C/Date: 26-Jan-1996 #sequence\_revision 26-Jan-1996 #text\_change 26-Jan-1996  
 C/Accession: D57444  
 R/Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.  
 J. Biol. Chem. 270, 21103-21108, 1995  
 A/Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the cric  
 A/Reference number: A57444; PMID:95403341; PMID:7673141  
 A/Accession: D57444  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-9 <LOR>

Query Match 25.4%; Score 16; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ERF 6  
 DB 3 ERF 5

Search completed: August 30, 2004, 10:58:51  
 Job time : 4.30743 secs



Thu Sep 2 07:41:40 2004

us-09-720-469a-6.aug30.rapb

Page 1

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:49:45 ; Search time 13.4527 Seconds  
(without alignments)  
257.253 Million cell updates/sec

Title: US-09-720-469a-6  
Perfect score: 63  
Sequence: 1 IYGERPDPNF 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1297172 seqs, 314612898 residues  
Total number of hits satisfying chosen parameters: 149443

Minimum DB seq length: 8  
Maximum DB seq length: 14

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: /cgn2\_6/prodata/1/pubppa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/prodata/1/pubppa/PCRT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/prodata/1/pubppa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/prodata/1/pubppa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/prodata/1/pubppa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/prodata/1/pubppa/PCRTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/prodata/1/pubppa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/prodata/1/pubppa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/prodata/1/pubppa/US09\_PUBCOMB.pep.\*  
10: /cgn2\_6/prodata/1/pubppa/US09C\_PUBCOMB.pep.\*  
11: /cgn2\_6/prodata/1/pubppa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/prodata/1/pubppa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/prodata/1/pubppa/US10\_PUBCOMB.pep.\*  
14: /cgn2\_6/prodata/1/pubppa/US10\_PUBCOMB.pep.\*  
15: /cgn2\_6/prodata/1/pubppa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/prodata/1/pubppa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/prodata/1/pubppa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/prodata/1/pubppa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	46.0	10	14	US-10-194-441A-7
2	28	44.4	8	14	US-10-226-629A-477
3	28	44.4	9	12	US-09-988-493-293
4	28	44.4	9	12	US-10-014-340-209
5	28	44.4	9	14	US-10-226-629A-478
6	28	44.4	9	14	US-10-226-629A-491
7	28	44.4	9	16	US-10-264-309-118
8	28	44.4	10	14	US-10-226-629A-479
9	28	44.4	10	14	US-10-226-629A-492
10	28	44.4	10	14	US-10-226-629A-505
11	28	44.4	11	14	US-10-226-629A-480
12	28	44.4	11	14	US-10-226-629A-493
13	28	44.4	11	14	US-10-226-629A-506
14	28	44.4	11	14	US-10-226-629A-518
15	28	44.4	12	14	US-10-286-457-432

16	28	44.4	12	14	US-10-226-629A-481	Sequence 481, App
17	28	44.4	12	14	US-10-226-629A-494	Sequence 494, App
18	28	44.4	12	14	US-10-226-629A-507	Sequence 507, App
19	28	44.4	12	14	US-10-226-629A-519	Sequence 519, App
20	28	44.4	12	14	US-10-226-629A-530	Sequence 530, App
21	28	44.4	13	14	US-10-226-629A-482	Sequence 482, App
22	28	44.4	13	14	US-10-226-629A-495	Sequence 495, App
23	28	44.4	13	14	US-10-226-629A-508	Sequence 508, App
24	28	44.4	13	14	US-10-226-629A-520	Sequence 520, App
25	28	44.4	13	14	US-10-226-629A-531	Sequence 531, App
26	28	44.4	13	14	US-10-226-629A-541	Sequence 541, App
27	28	44.4	14	14	US-10-226-629A-483	Sequence 483, App
28	28	44.4	14	14	US-10-226-629A-486	Sequence 486, App
29	28	44.4	14	14	US-10-226-629A-509	Sequence 509, App
30	28	44.4	14	14	US-10-226-629A-521	Sequence 521, App
31	28	44.4	14	14	US-10-226-629A-532	Sequence 532, App
32	28	44.4	14	14	US-10-226-629A-542	Sequence 542, App
33	28	44.4	14	14	US-10-226-629A-551	Sequence 551, App
34	27	42.9	8	14	US-10-226-629A-464	Sequence 464, App
35	27	42.9	9	14	US-10-226-629A-465	Sequence 465, App
36	27	42.9	10	10	US-09-572-404B-18	Sequence 18, Appl
37	27	42.9	10	14	US-10-226-629A-466	Sequence 466, App
38	27	42.9	11	14	US-10-226-629A-467	Sequence 467, App
39	27	42.9	12	14	US-10-254-446A-165	Sequence 165, App
40	27	42.9	12	14	US-10-226-629A-468	Sequence 468, App
41	27	42.9	13	14	US-10-226-629A-469	Sequence 469, App
42	27	42.9	14	14	US-10-226-629A-470	Sequence 470, App
43	26	41.3	8	15	US-10-149-138-2763	Sequence 2763, Ap
44	26	41.3	8	16	US-10-149-138-2763	Sequence 2763, Ap
45	26	41.3	10	10	US-09-572-404B-1153	Sequence 1153, Ap

# ALIGNMENTS

RESULT 1  
US-10-194-441A-7  
; Sequence 7, Application US/10194441A  
; Publication No. US20030148944A1  
; GENERAL INFORMATION:  
; APPLICANT: Holmdahl, Rickard  
; APPLICANT: Engstrom, Jan Ake  
; APPLICANT: Kihlberg, Jan  
; APPLICANT: Burkhardt, Harald  
; TITLE OF INVENTION: TRIPLE POLYPEPTIDE COMPLEXES  
; FILE REFERENCE: 11145-010001  
; CURRENT APPLICATION NUMBER: US/10/194,441A  
; CURRENT FILING DATE: 2002-07-11  
; PRIOR APPLICATION NUMBER: US 60/305,048  
; PRIOR FILING DATE: 2001-07-12  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-194-441A-7

Query Match 46.0%; Score 29; DB 14; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GERFP 7  
Db 6 GERFP 10

RESULT 2  
US-10-226-629A-477  
; Sequence 477, Application US/10226629A  
; Publication No. US20030166504A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.

```
APPLICANT: Morham, Scott
APPLICANT: Zavitz, Kenton
APPLICANT: Hobden, Adrian
TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
FILE REFERENCE: 5006.01
CURRENT APPLICATION NUMBER: US/10/226,629A
CURRENT FILING DATE: 2002-08-22
PRIOR APPLICATION NUMBER: US 60/314,182
PRIOR FILING DATE: 2001-08-22
NUMBER OF SEQ ID NOS: 736
SOFTWARE: PatentIn version 3.1
SEQ ID NO 477
LENGTH: 8
TYPE: PRT
ORGANISM: Variola virus
US-10-226-629A-477
```

```
Query Match      44.4%; Score 28; DB 14; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
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```
QY      4 ERPDPNF 11
      :|||
      1 KKYPDINF 8
```

```
RESULT 3
US-09-988-493-293
Sequence 293, Application US/09988493
Publication No. US20030064419A1
GENERAL INFORMATION:
APPLICANT: Herath, Herach Mudiyanselage Athula Chandrasiri
APPLICANT: O'Hare, Michael John
APPLICANT: Page, Martin John
APPLICANT: Parekh, Rajesh Bhikhu
APPLICANT: Waterfield, Michael Derek
TITLE OF INVENTION: Proteins, Genes, and Their Use for
FILE REFERENCE: 2543-1-024
CURRENT APPLICATION NUMBER: US/09/988,493
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: PCT/GB01/01219
PRIOR FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: GB 0006695.1
PRIOR FILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: GB 0007265.2
PRIOR FILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 308
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 293
LENGTH: 9
TYPE: PRT
ORGANISM: homo sapien
US-09-988-493-293
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```
Query Match      44.4%; Score 28; DB 12; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY      6 FPDENF 11
      :|||
      1 FEDENF 6
```

```
RESULT 4
US-10-014-340-209
Sequence 209, Application US/10014340
Publication No. US20030064411A1
GENERAL INFORMATION:
APPLICANT: Herath, et al
TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor, Including
FILE REFERENCE: 9195-078
```

```
CURRENT APPLICATION NUMBER: US/10/014,340
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 823
SOFTWARE: PatentIn version 3.0
SEQ ID NO 209
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-10-014-340-209
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```
Query Match      44.4%; Score 28; DB 12; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      6 FPDENF 11
      :|||
      1 FEDENF 6
```

```
RESULT 5
US-10-226-629A-478
Sequence 478, Application US/10226629A
Publication No. US20030166504A1
GENERAL INFORMATION:
APPLICANT: Myriad Genetics, Inc.
APPLICANT: Morham, Scott
APPLICANT: Zavitz, Kenton
APPLICANT: Hobden, Adrian
TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
FILE REFERENCE: 5006.01
CURRENT APPLICATION NUMBER: US/10/226,629A
CURRENT FILING DATE: 2002-08-22
PRIOR APPLICATION NUMBER: US 60/314,182
PRIOR FILING DATE: 2001-08-22
NUMBER OF SEQ ID NOS: 736
SOFTWARE: PatentIn version 3.1
SEQ ID NO 478
LENGTH: 9
TYPE: PRT
ORGANISM: Variola virus
US-10-226-629A-478
```

```
Query Match      44.4%; Score 28; DB 14; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      4 ERPDPNF 11
      :|||
      1 KKYPDINF 8
```

```
RESULT 6
US-10-226-629A-491
Sequence 491, Application US/10226629A
Publication No. US20030166504A1
GENERAL INFORMATION:
APPLICANT: Myriad Genetics, Inc.
APPLICANT: Morham, Scott
APPLICANT: Zavitz, Kenton
APPLICANT: Hobden, Adrian
TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
FILE REFERENCE: 5006.01
CURRENT APPLICATION NUMBER: US/10/226,629A
CURRENT FILING DATE: 2002-08-22
PRIOR APPLICATION NUMBER: US 60/314,182
PRIOR FILING DATE: 2001-08-22
NUMBER OF SEQ ID NOS: 736
SOFTWARE: PatentIn version 3.1
SEQ ID NO 491
LENGTH: 9
TYPE: PRT
ORGANISM: Variola virus
US-10-226-629A-491
```



Query Match 44.4%; Score 28; DB 14; Length 9;  
Best Local Similarity 50.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPDENF 11  
DB 2 KXYPLDNF 9

RESULT 7

US-10-264-309-118  
Sequence 118, Application US/10264309  
Publication No. US20040022794A1  
GENERAL INFORMATION:  
APPLICANT: DURHAM, L. KATHRYN  
APPLICANT: FRIEDMAN, DAVID L.  
APPLICANT: HERATH, HERATH  
APPLICANT: KIMMEL, LIDA H.  
APPLICANT: PAREKH, RAJESH B.  
APPLICANT: POTTER, DAVID M.  
APPLICANT: ROHLF, CHRISTIAN  
APPLICANT: SILBER, B. MICHAEL  
APPLICANT: SNYDER, PETER J.  
APPLICANT: SOARES, HOLLY D.  
APPLICANT: STIGER, THOMAS R.  
APPLICANT: SUNDERLAND, P. TREY  
APPLICANT: TOWNSEND, ROBERT R.  
APPLICANT: WHITE, W. FROST  
APPLICANT: WILLIAMS, STEPHEN A.  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR.  
TITLE OF INVENTION: INCLUDING DIAGNOSIS AND TREATMENT OF ALZHEIMER'S DISEASE  
FILE REFERENCE: POA-002.01  
CURRENT APPLICATION NUMBER: US/10/264.309  
CURRENT FILING DATE: 2002-10-03  
PRIOR APPLICATION NUMBER: 60/326,708  
PRIOR FILING DATE: 2001-10-03  
NUMBER OF SEQ ID NOS: 491  
SOFTWARE: PatentIn Version 2.1  
SEQ ID NO 118  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-264-309-118

Query Match 44.4%; Score 28; DB 16; Length 9;  
Best Local Similarity 83.3%; Pred. No. 1.2e+06;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 FPDFENF 11  
DB 1 FEDENF 6

RESULT 8  
US-10-226-629A-479  
Sequence 479, Application US/10226629A  
Publication No. US20030166504A1  
GENERAL INFORMATION:  
APPLICANT: Myriad Genetics, Inc.  
APPLICANT: Morham, Scott  
APPLICANT: ZAVITZ, Kenton  
APPLICANT: HODDEN, ADRIAN  
TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection  
FILE REFERENCE: 5006.01  
CURRENT APPLICATION NUMBER: US/10/226.629A  
CURRENT FILING DATE: 2002-08-22  
PRIOR APPLICATION NUMBER: US 60/314,182  
PRIOR FILING DATE: 2001-08-22  
NUMBER OF SEQ ID NOS: 736  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 479  
LENGTH: 10

TYPE: PRT  
ORGANISM: Variola virus  
US-10-226-629A-479

Query Match 44.4%; Score 28; DB 14; Length 10;  
Best Local Similarity 50.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPDENF 11  
DB 1 KXYPLDNF 8

RESULT 9  
US-10-226-629A-492  
Sequence 492, Application US/10226629A  
Publication No. US20030166504A1  
GENERAL INFORMATION:  
APPLICANT: Myriad Genetics, Inc.  
APPLICANT: Morham, Scott  
APPLICANT: ZAVITZ, Kenton  
APPLICANT: HODDEN, ADRIAN  
TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection  
FILE REFERENCE: 5006.01  
CURRENT APPLICATION NUMBER: US/10/226.629A  
CURRENT FILING DATE: 2002-08-22  
PRIOR APPLICATION NUMBER: US 60/314,182  
PRIOR FILING DATE: 2001-08-22  
NUMBER OF SEQ ID NOS: 736  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 492  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Variola virus  
US-10-226-629A-492

Query Match 44.4%; Score 28; DB 14; Length 10;  
Best Local Similarity 50.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPDENF 11  
DB 2 KXYPLDNF 9

RESULT 10  
US-10-226-629A-505  
Sequence 505, Application US/10226629A  
Publication No. US20030166504A1  
GENERAL INFORMATION:  
APPLICANT: Myriad Genetics, Inc.  
APPLICANT: Morham, Scott  
APPLICANT: ZAVITZ, Kenton  
APPLICANT: HODDEN, ADRIAN  
TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection  
FILE REFERENCE: 5006.01  
CURRENT APPLICATION NUMBER: US/10/226.629A  
CURRENT FILING DATE: 2002-08-22  
PRIOR APPLICATION NUMBER: US 60/314,182  
PRIOR FILING DATE: 2001-08-22  
NUMBER OF SEQ ID NOS: 736  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 505  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Variola virus  
US-10-226-629A-505

Query Match 44.4%; Score 28; DB 14; Length 10;  
Best Local Similarity 50.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPDENF 11

Db 3 KKYDPLNF 10

## RESULT 11

US-10-226-629A-480  
; Sequence 480, Application US/10226629A  
; Publication No. US20030166504A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavit, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection  
; FILE REFERENCE: 5006.01  
; CURRENT APPLICATION NUMBER: US/10/226,629A  
; CURRENT FILING DATE: 2002-08-22  
; PRIOR APPLICATION NUMBER: US 60/314,182  
; PRIOR FILING DATE: 2001-08-22  
; NUMBER OF SEQ ID NOS: 736  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 480  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Variola virus  
US-10-226-629A-480

Query Match 44.4%; Score 28; DB 14; Length 11;  
Best Local Similarity 50.0%; Pred. No. 2.7e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPDENF 11  
Db 1 KKYDPLNF 8

## RESULT 12

US-10-226-629A-493  
; Sequence 493, Application US/10226629A  
; Publication No. US20030166504A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavit, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection  
; FILE REFERENCE: 5006.01  
; CURRENT APPLICATION NUMBER: US/10/226,629A  
; CURRENT FILING DATE: 2002-08-22  
; PRIOR APPLICATION NUMBER: US 60/314,182  
; PRIOR FILING DATE: 2001-08-22  
; NUMBER OF SEQ ID NOS: 736  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 493  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Variola virus  
US-10-226-629A-493

Query Match 44.4%; Score 28; DB 14; Length 11;  
Best Local Similarity 50.0%; Pred. No. 2.7e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPDENF 11  
Db 2 KKYDPLNF 9

## RESULT 13

US-10-226-629A-506  
; Sequence 506, Application US/10226629A  
; Publication No. US20030166504A1  
; GENERAL INFORMATION:

; APPLICANT: Myriad Genetics, Inc.

; APPLICANT: Morham, Scott

; APPLICANT: Zavit, Kenton

; APPLICANT: Hobden, Adrian

; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection

; FILE REFERENCE: 5006.01

; CURRENT APPLICATION NUMBER: US/10/226,629A

; CURRENT FILING DATE: 2002-08-22

; PRIOR APPLICATION NUMBER: US 60/314,182

; PRIOR FILING DATE: 2001-08-22

; NUMBER OF SEQ ID NOS: 736

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 506

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Variola virus

US-10-226-629A-506

QY 4 ERFPDENF 11  
Db 3 KKYDPLNF 10

## RESULT 14

US-10-226-629A-518  
; Sequence 518, Application US/10226629A  
; Publication No. US20030166504A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavit, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection  
; FILE REFERENCE: 5006.01  
; CURRENT APPLICATION NUMBER: US/10/226,629A  
; CURRENT FILING DATE: 2002-08-22  
; PRIOR APPLICATION NUMBER: US 60/314,182  
; PRIOR FILING DATE: 2001-08-22  
; NUMBER OF SEQ ID NOS: 736  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 518  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Variola virus  
US-10-226-629A-518

Query Match 44.4%; Score 28; DB 14; Length 11;  
Best Local Similarity 50.0%; Pred. No. 2.7e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPDENF 11  
Db 4 KKYDPLNF 11

## RESULT 15

US-10-286-457-432  
; Sequence 432, Application US/10286457  
; Publication No. US20030166504A1  
; GENERAL INFORMATION:  
; APPLICANT: JENO GYURIS et al.  
; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY  
; FILE REFERENCE: GPCI-P01-178  
; CURRENT APPLICATION NUMBER: US/10/286,457  
; CURRENT FILING DATE: 2002-11-01  
; PRIOR APPLICATION NUMBER: 60/334822  
; PRIOR FILING DATE: 2001-11-01  
; NUMBER OF SEQ ID NOS: 684  
; SOFTWARE: PatentIn version 3.1

SEQ ID NO 432  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: artificial sequence isolated from random peptide libraries, based  
OTHER INFORMATION: ability to selectively bind to endothelial cells  
US-10-286-457-432

Query Match 44.4%; Score 28; DB 14; Length 12;  
Best Local Similarity 57.1%; Pred. No. 2.9e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 IYGERFP 7  
Db 3 VYGNRLP 9

RESULT 16  
US-10-226-629A-481  
Sequence 481, Application US/10226629A  
Publication No. US20030166504A1  
GENERAL INFORMATION:  
APPLICANT: Myriad Genetics, Inc.  
APPLICANT: Morham, Scott  
APPLICANT: Zavitz, Kenton  
APPLICANT: Hobden, Adrian  
TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection  
FILE REFERENCE: 5006.01  
CURRENT APPLICATION NUMBER: US/0/226,629A  
CURRENT FILING DATE: 2002-08-22  
PRIOR APPLICATION NUMBER: US 60/314,182  
PRIOR FILING DATE: 2001-08-22  
NUMBER OF SEQ ID NOS: 736  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 481  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Variola virus  
US-10-226-629A-481

Query Match 44.4%; Score 28; DB 14; Length 12;  
Best Local Similarity 50.0%; Pred. No. 2.9e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERPPDENF 11  
Db 1 KKYDPLNF 8

RESULT 17  
US-10-226-629A-494  
Sequence 494, Application US/10226629A  
Publication No. US20030166504A1  
GENERAL INFORMATION:  
APPLICANT: Myriad Genetics, Inc.  
APPLICANT: Morham, Scott  
APPLICANT: Zavitz, Kenton  
APPLICANT: Hobden, Adrian  
TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection  
FILE REFERENCE: 5006.01  
CURRENT APPLICATION NUMBER: US/10/226,629A  
CURRENT FILING DATE: 2002-08-22  
PRIOR APPLICATION NUMBER: US 60/314,182  
PRIOR FILING DATE: 2001-08-22  
NUMBER OF SEQ ID NOS: 736  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 494  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Variola virus  
US-10-226-629A-494

Query Match 44.4%; Score 28; DB 14; Length 12;  
Best Local Similarity 50.0%; Pred. No. 2.9e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERPPDENF 11  
Db 2 KKYDPLNF 9

RESULT 18  
US-10-226-629A-507  
Sequence 507, Application US/10226629A  
Publication No. US20030166504A1  
GENERAL INFORMATION:  
APPLICANT: Myriad Genetics, Inc.  
APPLICANT: Morham, Scott  
APPLICANT: Zavitz, Kenton  
APPLICANT: Hobden, Adrian  
TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection  
FILE REFERENCE: 5006.01  
CURRENT APPLICATION NUMBER: US/10/226,629A  
CURRENT FILING DATE: 2002-08-22  
PRIOR APPLICATION NUMBER: US 60/314,182  
PRIOR FILING DATE: 2001-08-22  
NUMBER OF SEQ ID NOS: 736  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 507  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Variola virus  
US-10-226-629A-507

Query Match 44.4%; Score 28; DB 14; Length 12;  
Best Local Similarity 50.0%; Pred. No. 2.9e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERPPDENF 11  
Db 3 KKYDPLNF 10

RESULT 19  
US-10-226-629A-519  
Sequence 519, Application US/10226629A  
Publication No. US20030166504A1  
GENERAL INFORMATION:  
APPLICANT: Myriad Genetics, Inc.  
APPLICANT: Morham, Scott  
APPLICANT: Zavitz, Kenton  
APPLICANT: Hobden, Adrian  
TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection  
FILE REFERENCE: 5006.01  
CURRENT APPLICATION NUMBER: US/10/226,629A  
CURRENT FILING DATE: 2002-08-22  
PRIOR APPLICATION NUMBER: US 60/314,182  
PRIOR FILING DATE: 2001-08-22  
NUMBER OF SEQ ID NOS: 736  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 519  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Variola virus  
US-10-226-629A-519

Query Match 44.4%; Score 28; DB 14; Length 12;  
Best Local Similarity 50.0%; Pred. No. 2.9e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERPPDENF 11  
Db 4 KKYDPLNF 11

```
RESULT 20
US-10-226-629A-530
; Sequence 530, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; PRIOR FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 530
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-530

Query Match          44.4%; Score 28; DB 14; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFDPENF 11
Db 5 KKYDPLNF 12

RESULT 21
US-10-226-629A-482
; Sequence 482, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; PRIOR FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 482
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-482

Query Match          44.4%; Score 28; DB 14; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFDPENF 11
Db 1 KKYDPLNF 8

RESULT 22
US-10-226-629A-495
; Sequence 495, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; PRIOR FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 495
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-495

Query Match          44.4%; Score 28; DB 14; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFDPENF 11
Db 2 KKYDPLNF 9

RESULT 23
US-10-226-629A-508
; Sequence 508, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; PRIOR FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 508
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-508

Query Match          44.4%; Score 28; DB 14; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFDPENF 11
Db 3 KKYDPLNF 10

RESULT 24
US-10-226-629A-520
; Sequence 520, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; PRIOR FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 520
```

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LENGTH: 13  
TYPE: PRT  
ORGANISM: Variola virus  
US-10-226-629A-520

Query Match 44.4%; Score 28; DB 14; Length 13;  
Best Local Similarity 50.0%; Pred. No. 3.2e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPDENF 11  
DB 4 KKYPDLNF 11

RESULT 25:

US-10-226-629A-531  
Sequence 531, Application US/10226629A  
Publication No. US20030166504A1  
GENERAL INFORMATION:  
APPLICANT: Myriad Genetics, Inc.  
APPLICANT: Morham, Scott  
APPLICANT: Zavitz, Kenton  
APPLICANT: Hobden, Adrian  
TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection  
FILE REFERENCE: 5006.01  
CURRENT APPLICATION NUMBER: US/10/226,629A  
CURRENT FILING DATE: 2002-08-22  
PRIOR APPLICATION NUMBER: US 60/314,182  
PRIOR FILING DATE: 2001-08-22  
NUMBER OF SEQ ID NOS: 736  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 531  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Variola virus  
US-10-226-629A-531

Query Match 44.4%; Score 28; DB 14; Length 13;  
Best Local Similarity 50.0%; Pred. No. 3.2e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPDENF 11  
DB 5 KKYPDLNF 12

RESULT 26:

US-10-226-629A-541  
Sequence 541, Application US/10226629A  
Publication No. US20030166504A1  
GENERAL INFORMATION:  
APPLICANT: Myriad Genetics, Inc.  
APPLICANT: Morham, Scott  
APPLICANT: Zavitz, Kenton  
APPLICANT: Hobden, Adrian  
TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection  
FILE REFERENCE: 5006.01  
CURRENT APPLICATION NUMBER: US/10/226,629A  
CURRENT FILING DATE: 2002-08-22  
PRIOR APPLICATION NUMBER: US 60/314,182  
PRIOR FILING DATE: 2001-08-22  
NUMBER OF SEQ ID NOS: 736  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 541  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Variola virus  
US-10-226-629A-541

Query Match 44.4%; Score 28; DB 14; Length 13;  
Best Local Similarity 50.0%; Pred. No. 3.2e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPDENF 11  
DB 6 KKYPDLNF 13

RESULT 27:

US-10-226-629A-483  
Sequence 483, Application US/10226629A  
Publication No. US20030166504A1  
GENERAL INFORMATION:  
APPLICANT: Myriad Genetics, Inc.  
APPLICANT: Morham, Scott  
APPLICANT: Zavitz, Kenton  
APPLICANT: Hobden, Adrian  
TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection  
FILE REFERENCE: 5006.01  
CURRENT APPLICATION NUMBER: US/10/226,629A  
CURRENT FILING DATE: 2002-08-22  
PRIOR APPLICATION NUMBER: US 60/314,182  
PRIOR FILING DATE: 2001-08-22  
NUMBER OF SEQ ID NOS: 736  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 483  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Variola virus  
US-10-226-629A-483

Query Match 44.4%; Score 28; DB 14; Length 14;  
Best Local Similarity 50.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPDENF 11  
DB 1 KKYPDLNF 8

RESULT 28:

US-10-226-629A-496  
Sequence 496, Application US/10226629A  
Publication No. US20030166504A1  
GENERAL INFORMATION:  
APPLICANT: Myriad Genetics, Inc.  
APPLICANT: Morham, Scott  
APPLICANT: Zavitz, Kenton  
APPLICANT: Hobden, Adrian  
TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection  
FILE REFERENCE: 5006.01  
CURRENT APPLICATION NUMBER: US/10/226,629A  
CURRENT FILING DATE: 2002-08-22  
PRIOR APPLICATION NUMBER: US 60/314,182  
PRIOR FILING DATE: 2001-08-22  
NUMBER OF SEQ ID NOS: 736  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 496  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Variola virus  
US-10-226-629A-496

Query Match 44.4%; Score 28; DB 14; Length 14;  
Best Local Similarity 50.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPDENF 11  
DB 2 KKYPDLNF 9

RESULT 29:

US-10-226-629A-509  
Sequence 509, Application US/10226629A  
Publication No. US20030166504A1

```

; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; PRIOR FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 509
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-509

Query Match      44.4%; Score 28; DB 14; Length 14;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      4 ERFPDENF 11
      ::|||
Db      3 KKYDPDINF 10

RESULT 30
US-10-226-629A-521
; Sequence 521, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; PRIOR FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 521
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-521

Query Match      44.4%; Score 28; DB 14; Length 14;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      4 ERFPDENF 11
      ::|||
Db      4 KKYDPDINF 11

RESULT 31
US-10-226-629A-532
; Sequence 532, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; PRIOR FILING DATE: 2002-08-22
```

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; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 532
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-532

Query Match      44.4%; Score 28; DB 14; Length 14;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      4 ERFPDENF 11
      ::|||
Db      5 KKYDPDINF 12

RESULT 32
US-10-226-629A-542
; Sequence 542, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; PRIOR FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 542
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-542

Query Match      44.4%; Score 28; DB 14; Length 14;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      4 ERFPDENF 11
      ::|||
Db      6 KKYDPDINF 13

RESULT 33
US-10-226-629A-551
; Sequence 551, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; PRIOR FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 551
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-551
```

Query Match 44.4%; Score 28; DB 14; Length 14;  
Best Local Similarity 50.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 RPPDENE 11  
DB 7 KYPDLNF 14

RESULT 34  
US-10-226-629A-464  
; Sequence 464, Application US/10226629A  
; Publication No. US20030166504A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection  
; FILE REFERENCE: 5006.01  
; CURRENT APPLICATION NUMBER: US/10/226,629A  
; CURRENT FILING DATE: 2002-08-22  
; PRIOR APPLICATION NUMBER: US 60/314,182  
; PRIOR FILING DATE: 2001-08-22  
; NUMBER OF SEQ ID NOS: 736  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 464  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Variola virus  
US-10-226-629A-464

Query Match 42.9%; Score 27; DB 14; Length 8;  
Best Local Similarity 57.1%; Pred. No. 1.2e+06;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 RPPDENE 11  
DB 1 KYPDLNF 7

RESULT 35  
US-10-226-629A-465  
; Sequence 465, Application US/10226629A  
; Publication No. US20030166504A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection  
; FILE REFERENCE: 5006.01  
; CURRENT APPLICATION NUMBER: US/10/226,629A  
; CURRENT FILING DATE: 2002-08-22  
; PRIOR APPLICATION NUMBER: US 60/314,182  
; PRIOR FILING DATE: 2001-08-22  
; NUMBER OF SEQ ID NOS: 736  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 465  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Variola virus  
US-10-226-629A-465

Query Match 42.9%; Score 27; DB 14; Length 9;  
Best Local Similarity 57.1%; Pred. No. 1.2e+06;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 RPPDENE 11  
DB 1 KYPDLNF 7

RESULT 36  
US-09-572-404B-18  
; Sequence 18, Application US/09572404B  
; Publication No. US20030078374A1  
; GENERAL INFORMATION:  
; APPLICANT: Proteom Ltd  
; TITLE OF INVENTION: Complementary peptide ligands from the human genome  
; FILE REFERENCE: Human Patent  
; CURRENT APPLICATION NUMBER: US/09/572,404B  
; CURRENT FILING DATE: 2000-05-17  
; NUMBER OF SEQ ID NOS: 4203  
; SOFTWARE: Protpatent version 1.0  
; SEQ ID NO 18  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; OTHER INFORMATION: Sequence located in DSC3 OR DSC4 at 716-725 and may interact with  
US-09-572-404B-18

Query Match 42.9%; Score 27; DB 10; Length 10;  
Best Local Similarity 66.7%; Pred. No. 3.6e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 GRRPFD 8  
DB 5 GRRPFD 10

RESULT 37  
US-10-226-629A-466  
; Sequence 466, Application US/10226629A  
; Publication No. US20030166504A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection  
; FILE REFERENCE: 5006.01  
; CURRENT APPLICATION NUMBER: US/10/226,629A  
; CURRENT FILING DATE: 2002-08-22  
; PRIOR APPLICATION NUMBER: US 60/314,182  
; PRIOR FILING DATE: 2001-08-22  
; NUMBER OF SEQ ID NOS: 736  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 466  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Variola virus  
US-10-226-629A-466

Query Match 42.9%; Score 27; DB 14; Length 10;  
Best Local Similarity 57.1%; Pred. No. 3.6e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 RPPDENE 11  
DB 1 KYPDLNF 7

RESULT 38  
US-10-226-629A-467  
; Sequence 467, Application US/10226629A  
; Publication No. US20030166504A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection

```

; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 467
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-467

Query Match
Best Local Similarity 57.1%; Score 27; DB 14; Length 11;
Pred. No. 4e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 RPPDNF 11
Db 1 KYPDLP 7

RESULT 39
US-10-254-446A-165
; Sequence 165, Application US/10254446A
; Publication No. US20030113714A1
; GENERAL INFORMATION:
; APPLICANT: Belcher, Angela M
; APPLICANT: Smalley, Richard E.
; APPLICANT: Ryan, Esther
; APPLICANT: Lee, Seung-Wuk
; TITLE OF INVENTION: BIOLOGICAL CONTROL OF NANOPARTICLES
; FILE REFERENCE: 119927-1066
; CURRENT APPLICATION NUMBER: US/10/254,446A
; CURRENT FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: 60/325,664
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 245
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 165
; LENGTH: 12
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURES:
; OTHER INFORMATION: peptide with peptide binding sequence retrieved from phage biopar
US-10-254-446A-165

Query Match
Best Local Similarity 42.9%; Score 27; DB 14; Length 12;
Pred. No. 4.4e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 IYGRFPD 8
Db 1 LMGRRPD 8

RESULT 40
US-10-226-629A-468
; Sequence 468, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; ORGANISM: Variola virus

; SEQ ID NO 468
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-468

Query Match
Best Local Similarity 42.9%; Score 27; DB 14; Length 12;
Pred. No. 4.4e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 RPPDNF 11
Db 1 KYPDLP 7

RESULT 41
US-10-226-629A-469
; Sequence 469, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 469
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-469

Query Match
Best Local Similarity 42.9%; Score 27; DB 14; Length 13;
Pred. No. 4.8e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 RPPDNF 11
Db 1 KYPDLP 7

RESULT 42
US-10-226-629A-470
; Sequence 470, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 470
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-470

Query Match
Best Local Similarity 42.9%; Score 27; DB 14; Length 14;
Pred. No. 5.2e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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QY 5 RFPDEF 11  
Db 1 KYPDLNF 7

## RESULT 43

US-10-149-138-2763  
; Sequence 2763, Application US/10149138  
; Publication No. US20040018971A1  
; GENERAL INFORMATION:  
; APPLICANT: Fikes, John  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Sidney, John  
; APPLICANT: Southwood, Scott  
; APPLICANT: Chesnut, Robert  
; APPLICANT: Celis, Esteban  
; APPLICANT: Keogh, Elissa  
; TITLE OF INVENTION: Inducing Cellular Immune Responses to  
; FILE REFERENCE: 2060.0140001  
; CURRENT APPLICATION NUMBER: US/10/149,138  
; CURRENT FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: PCT/US00/33591  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: US 09/458,299  
; PRIOR FILING DATE: 1999-12-11  
; NUMBER OF SEQ ID NOS: 4641  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2763  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-2763

Query Match 41.3%; Score 26; DB 15; Length 8;  
Best Local Similarity 80.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 RFPDE 9  
Db 1 KFPDE 5

## RESULT 44

US-10-149-138-2763  
; Sequence 2763, Application US/10149138  
; Publication No. US20040121946A9  
; GENERAL INFORMATION:  
; APPLICANT: Fikes, John  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Sidney, John  
; APPLICANT: Southwood, Scott  
; APPLICANT: Chesnut, Robert  
; APPLICANT: Celis, Esteban  
; APPLICANT: Keogh, Elissa  
; TITLE OF INVENTION: Inducing Cellular Immune Responses to  
; FILE REFERENCE: 2060.0140001  
; CURRENT APPLICATION NUMBER: US/10/149,138  
; CURRENT FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: PCT/US00/33591  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: US 09/458,299  
; PRIOR FILING DATE: 1999-12-11  
; NUMBER OF SEQ ID NOS: 4641  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2763  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-2763

Query Match 41.3%; Score 26; DB 16; Length 8;  
Best Local Similarity 80.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 RFPDE 9  
Db 1 KFPDE 5

## RESULT 45

US-09-572-404B-1153  
; Sequence 1153, Application US/09572404B  
; Publication No. US20030078374A1  
; GENERAL INFORMATION:  
; APPLICANT: Proteom Ltd  
; TITLE OF INVENTION: Complementary peptide ligands from the human genome  
; FILE REFERENCE: Human Patent  
; CURRENT APPLICATION NUMBER: US/09/572,404B  
; CURRENT FILING DATE: 2000-05-17  
; NUMBER OF SEQ ID NOS: 4203  
; SOFTWARE: ProoPatent version 1.0  
; SEQ ID NO 1153  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; OTHER INFORMATION: sequence located in BTN at 177-186 and may interact with Sequence  
US-09-572-404B-1153

Query Match 41.3%; Score 26; DB 10; Length 10;  
Best Local Similarity 80.0%; Pred. No. 5.4e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GERFP 7  
Db 6 GERFP 10

Search completed: August 30, 2004, 11:04:58  
Job time : 14.4527 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:59 / Search time 4.34797 Seconds  
(without alignments)  
130.609 Million cell updates/sec

Title: US-09-720-469A-6  
Perfect score: 63  
Sequence: 1 IYGERFPDENP 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 78885

Minimum DB seq length: 8  
Maximum DB seq length: 14

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA: \*  
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2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pdp: \*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pdp: \*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pdp: \*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	47.6	10	2	US-08-658-639-8
2	30	47.6	10	3	US-08-944-604-8
3	29	46.0	12	2	US-08-432-871C-99
4	29	46.0	12	4	US-09-270-956-99
5	28	44.4	13	1	US-07-923-724-57
6	28	44.4	13	2	US-08-609-426A-57
7	28	44.4	13	2	US-08-374-652C-44
8	27	42.9	12	4	US-08-634-332A-77
9	25	39.7	9	1	US-08-215-805A-77
10	25	39.7	9	1	US-08-215-805A-44
11	25	39.7	9	1	US-08-278-091-23
12	25	39.7	11	1	US-08-483-859-23
13	25	39.7	11	1	US-08-472-173-23
14	25	39.7	11	1	US-08-487-167-23
15	25	39.7	11	2	US-08-482-816-23
16	25	39.7	11	2	US-08-296-149-23
17	25	39.7	11	2	US-08-801-499-23
18	25	39.7	11	2	US-08-815-271-23
19	25	39.7	11	2	US-08-609-426A-57
20	25	39.7	11	3	US-09-074-650-23
21	25	39.7	11	3	US-09-074-650-23
22	25	39.7	11	3	US-09-106-468-23
23	25	39.7	11	3	US-09-106-466A-23
24	25	39.7	11	3	US-09-106-467-23
25	25	39.7	13	4	US-08-945-168-95
26	25	39.7	13	4	US-08-999-689A-9
27	25	39.7	14	2	US-08-945-168-94

28	24	38.1	8	3	US-07-861-458C-115	Sequence 115, App
29	24	38.1	9	2	US-08-569-166-23	Sequence 23, App1
30	24	38.1	9	2	US-08-522-269B-6	Sequence 6, App1
31	24	38.1	9	3	US-09-294-923-6	Sequence 59, App1
32	24	38.1	9	3	US-08-960-780-59	Sequence 59, App1
33	24	38.1	9	3	US-09-073-898-59	Sequence 65, App1
34	24	38.1	9	3	US-09-518-046-65	Sequence 79, App1
35	24	38.1	9	3	US-09-518-046-65	Sequence 144, App
36	24	38.1	9	3	US-09-618-259-51	Sequence 51, App1
37	24	38.1	9	4	US-09-618-259-51	Sequence 70, App1
38	24	38.1	9	4	US-09-618-259-51	Sequence 59, App1
39	24	38.1	10	1	US-08-151-574-3	Sequence 3, App1
40	24	38.1	10	1	US-08-300-386A-59	Sequence 59, App1
41	24	38.1	10	2	US-08-419-448-3	Sequence 3, App1
42	24	38.1	10	2	US-08-931-648-59	Sequence 59, App1
43	24	38.1	10	3	US-09-233-510-3	Sequence 3, App1
44	24	38.1	10	4	PCT-US93-08067-4	Sequence 4, App1
45	24	38.1	10	5		

ALIGNMENTS

RESULT 1  
US-08-658-639-8  
Sequence 8, Application US/08658639  
Patent No. 5914238  
GENERAL INFORMATION:  
APPLICANT: KESSEE, SUSAN  
APPLICANT: OBAR, ROBERT  
TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF  
TITLE OF INVENTION: BREAST CANCER  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Tesca, Hurwitz & Thibault  
STREET: 125 High St.  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/658,639  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: MEYERS, THOMAS C  
REGISTRATION NUMBER: 36,989  
REFERENCE/DOCKET NUMBER: MTP-021 (8395/24)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-658-639-8

Query Match 47.6%; Score 30; DB 2; Length 10;  
Best Local Similarity 71.4%; Pred. No. 40;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Caps 0;  
Oy 5 RFPDENP 11  
Db 1 KFDDENF 7

RESULT 2  
US-08-944-604-8  
Sequence 8, Application US/08944604  
Patent No. 621811  
GENERAL INFORMATION:  
APPLICANT: KEESSE, SUSAN  
APPLICANT: OBAR, ROBERT  
APPLICANT: WU, YING-JYE  
TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF  
TITLE OF INVENTION: BREAST CANCER  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Testa, Hurwitz & Thibault  
STREET: 125 High St.  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/944,604  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MEYERS, THOMAS C  
REGISTRATION NUMBER: 36,989  
REFERENCE/DOCKET NUMBER: MTP-021 (8395/24)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-944-604-8  
Query Match 47.6%; Score 30; DB 3; Length 10;  
Best Local Similarity 71.4%; Pred. No. 40;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
CY 5 REPDPENF 11  
DB 1 KFDDENF 7  
RESULT 3  
US-08-432-871C-99  
Sequence 99, Application US/08432871C  
Patent No. 5877010  
GENERAL INFORMATION:  
APPLICANT: Loeb, Lawrence A.  
APPLICANT: Black, Margaret E.  
TITLE OF INVENTION: THYMIDINE KINASE MUTANTS  
NUMBER OF SEQUENCES: 104  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/432,871C  
FILING DATE: 02-MAY-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: McMASTERS, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 240052.409C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
TELEX: 3723836  
INFORMATION FOR SEQ ID NO: 99:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-432-871C-99  
Query Match 46.0%; Score 29; DB 2; Length 12;  
Best Local Similarity 50.0%; Pred. No. 71;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
CY 2 YGERPDPENF 11  
DB 2 WGRDRPIEXF 11  
RESULT 4  
US-09-270-956-99  
Sequence 99, Application US/09270956  
Patent No. 6451571  
GENERAL INFORMATION:  
APPLICANT: Loeb, Lawrence A.  
APPLICANT: Black, Margaret E.  
TITLE OF INVENTION: THYMIDINE KINASE MUTANTS  
NUMBER OF SEQUENCES: 104  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED AND BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/270,956  
FILING DATE: 17-MAR-1999  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: McMASTERS, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 240052.409C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
TELEX: 3723836  
INFORMATION FOR SEQ ID NO: 99:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-09-270-956-99  
Query Match 46.0%; Score 29; DB 4; Length 12;  
Best Local Similarity 50.0%; Pred. No. 71;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 YGERPDPENF 11  
:|||||  
Db 2 WGRHPLEKF 11

## RESULT 5

US-07-923-724-57  
; Sequence 57, Application US/07923724  
; Patent No. 5780292  
; GENERAL INFORMATION:  
; APPLICANT: Nevalainen, Helena K.M.  
; APPLICANT: Paloheimo, Marja T.  
; APPLICANT: Miettinen-Oinonen, Arja S.K.  
; APPLICANT: Torkkeli, Tuula K.  
; APPLICANT: Cantrell, Michael  
; APPLICANT: Piddington, Christopher S.  
; APPLICANT: Rambosek, John A.  
; APPLICANT: Turunen, Marja K.  
; APPLICANT: Fagerstr m, Richard B.  
; TITLE OF INVENTION: Production of Phytase Degrading Enzymes  
; TITLE OF INVENTION: in Trichoderma  
; NUMBER OF SEQUENCES: 66  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/923,724  
; FILING DATE: 31-JUL-1992  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/496,155  
; FILING DATE: 19-MAR-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/044,077  
; FILING DATE: 29-APR-1987  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: UK 8610600  
; FILING DATE: 30-APR-1986  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cimbal, Michele A.  
; REGISTRATION NUMBER: 33,851  
; REFERENCE/DOCKET NUMBER: 1050.0240004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 57:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 amino acids  
; TYPE: amino acid  
; TOPOLOGY: both  
US-07-923-724-57

Query Match 44.4%; Score 28; DB 1; Length 13;  
Best Local Similarity 66.7%; Pred. No. 1.1e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGERFP 7  
:|||||  
Db 2 HGERYP 7

RESULT 6  
US-08-609-426A-57

; Sequence 57, Application US/08609426A  
; Patent No. 5830733  
; GENERAL INFORMATION:  
; APPLICANT: Nevalainen, Helena K.M.  
; APPLICANT: Paloheimo, Marja T.  
; APPLICANT: Miettinen-Oinonen, Arja S.K.  
; APPLICANT: Torkkeli, Tuula K.  
; APPLICANT: Cantrell, Michael  
; APPLICANT: Piddington, Christopher S.  
; APPLICANT: Rambosek, John A.  
; APPLICANT: Turunen, Marja K.  
; APPLICANT: Fagerstr m, Richard B.  
; APPLICANT: Houston, Christine S.  
; TITLE OF INVENTION: Production of Phytase Degrading Enzymes  
; TITLE OF INVENTION: in Trichoderma  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/609,426A  
; FILING DATE: 01-MAR-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/923,724  
; FILING DATE: 31-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/496,155  
; FILING DATE: 19-MAR-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/044,077  
; FILING DATE: 29-APR-1987  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: UK 8610600  
; FILING DATE: 30-APR-1986  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Reed, Grant E.  
; REGISTRATION NUMBER: P-41,264  
; REFERENCE/DOCKET NUMBER: 1050.0080001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 57:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 amino acids  
; TYPE: amino acid  
; TOPOLOGY: both  
US-08-609-426A-57

Query Match 44.4%; Score 28; DB 2; Length 13;  
Best Local Similarity 66.7%; Pred. No. 1.1e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGERFP 7  
:|||||  
Db 2 HGERYP 7

RESULT 7  
US-08-374-652C-44  
; Sequence 44, Application US/08374652C  
; Patent No. 5834286  
; GENERAL INFORMATION:  
; APPLICANT: NEVALAINEN, HELENA K.M.

APPLICANT: PALOHEIMO, MARIA T.  
APPLICANT: RAGERSTROM, RICHARD B.  
APPLICANT: MIETTINEN-OINONEN, ARAA S.  
APPLICANT: TURUNEN, MARCA K.  
APPLICANT: RAMBOSK, JOHN A.  
APPLICANT: RIDDINGTON, CHRISTOPHER S.  
APPLICANT: HOUSTON, CHRISTINE S.  
APPLICANT: CANTRELL, MICHAEL A.  
TITLE OF INVENTION: RECOMBINANT CELLS, DNA CONSTRUCTS,  
TITLE OF INVENTION: VECTORS AND METHODS FOR EXPRESSING PHYTATE DEGRADING  
TITLE OF INVENTION: ENZYMES IN DESIRED RATIOS  
NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 NEW YORK AVENUE, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/374,652C  
FILING DATE: 24-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/07058  
FILING DATE: 27-JUL-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/925,401  
FILING DATE: 31-JUL-1992  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: REED, GRANT E.  
REGISTRATION NUMBER: 41,264  
REFERENCE/DOCKET NUMBER: 1050.071001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 44:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide  
US-08-374-652C-44

Query Match 44.4%; Score 28; DB 2; Length 13;  
Best Local Similarity 66.7%; Pred. No. 1.1e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YGERFP 7  
:||||:  
Db 2 HGERYP 7

RESULT 8  
US-08-634-332A-77  
Sequence 77, Application US/08634332A  
Patent No. 6531578  
GENERAL INFORMATION:  
APPLICANT: ROBERT WEBBER  
TITLE OF INVENTION: IMMUNOASSAY METHOD EMPLOYING  
MONOCLONAL ANTIBODY REACTIVE TO HUMAN INOS  
NUMBER OF SEQUENCES: 85  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIELEN, PETERSON & LAMPE  
STREET: 1990 N. CALIFORNIA BOULEVARD, SUITE 720

CITY: WALNUT CREEK  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94596  
COMPUTER READABLE FORM:  
MEDIUM TYPE: IBM PC COMPATIBLE  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: MICROSOFT WORD  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/634,332A  
FILING DATE: 12-APR-1996  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: NONE  
FILING DATE: NONE  
ATTORNEY/AGENT INFORMATION:  
NAME: THEODORE J. BIELEN, JR.  
REGISTRATION NUMBER: 27,420  
REFERENCE/DOCKET NUMBER: 12280  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (925) 937-1515  
TELEFAX: (925) 937-1529  
INFORMATION FOR SEQ ID NO: 77:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
NAME/KEY: HUMAN INOS (1015-1026)  
LOCATION: CARBOXY TERMINAL WITH AMIDE  
IDENTIFICATION METHOD: AMINO ACID ANALYSIS  
OTHER INFORMATION:  
SEQUENCE DESCRIPTION: SEQ ID NO: 77:  
US-08-634-332A-77

Query Match 42.9%; Score 27; DB 4; Length 12;  
Best Local Similarity 62.5%; Pred. No. 1.6e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GERPDEN 10  
:||||:  
Db 1 GSRPDED 8

RESULT 9  
US-08-215-805A-27  
Sequence 27, Application US/08215805A  
Patent No. 5559008  
GENERAL INFORMATION:  
APPLICANT: GRANG, YUNG-FU  
TITLE OF INVENTION: LEUKOTOXIN GENE FROM PASTURELLA  
TITLE OF INVENTION: SUI5  
NUMBER OF SEQUENCES: 84  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE  
STREET: Clinton Square, P.O. Box 1051  
CITY: Rochester  
STATE: New York  
COUNTRY: USA  
ZIP: 14603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/215,805A  
FILING DATE: 22-MAR-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: TIMIAN, SUSAN J.  
REGISTRATION NUMBER: 34,103

REFERENCE/DOCKET NUMBER: 19603/61 (D-1329A)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (716) 263-1636  
TELEFAX: (716) 263-1600  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Actinobacillus actinomycetemcomitans  
US-08-215-805A-27

Query Match 39.7%; Score 25; DB 1; Length 9;  
Best Local Similarity 57.1%; Pred. No. 3e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YGERFPD 8  
Db 2 YGSKFND 8

RESULT 10  
US-08-215-805A-44  
Sequence 44, Application US/08215805A  
Patent No. 5559008  
GENERAL INFORMATION:  
APPLICANT: Chang, Yung-Fu  
TITLE OF INVENTION: LEUKOTOXIN GENE FROM PASTEURRELLA  
TITLE OF INVENTION: SUI5  
NUMBER OF SEQUENCES: 84  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon, Hargrave, Devans & Doyle  
STREET: Clinton Square, P.O. Box 1051  
CITY: Rochester  
STATE: New York  
COUNTRY: USA  
ZIP: 14603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/215,805A  
FILING DATE: 22-MAR-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Timian, Susan J.  
REGISTRATION NUMBER: 34,103  
REFERENCE/DOCKET NUMBER: 19603/61 (D-1329A)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (716) 263-1636  
TELEFAX: (716) 263-1600  
INFORMATION FOR SEQ ID NO: 44:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Actinobacillus pleuropneumoniae  
US-08-215-805A-44

Query Match 39.7%; Score 25; DB 1; Length 9;  
Best Local Similarity 44.4%; Pred. No. 3e+05;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 1 YGERFPD 9  
:|:|:|

Db 1 LYGDKGNDE 9

RESULT 11  
US-08-215-805A-54  
Sequence 54, Application US/08215805A  
Patent No. 5559008  
GENERAL INFORMATION:  
APPLICANT: Chang, Yung-Fu  
TITLE OF INVENTION: LEUKOTOXIN GENE FROM PASTEURRELLA  
TITLE OF INVENTION: SUI5  
NUMBER OF SEQUENCES: 84  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon, Hargrave, Devans & Doyle  
STREET: Clinton Square, P.O. Box 1051  
CITY: Rochester  
STATE: New York  
COUNTRY: USA  
ZIP: 14603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/215,805A  
FILING DATE: 22-MAR-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Timian, Susan J.  
REGISTRATION NUMBER: 34,103  
REFERENCE/DOCKET NUMBER: 19603/61 (D-1329A)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (716) 263-1636  
TELEFAX: (716) 263-1600  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Actinobacillus pleuropneumoniae  
US-08-215-805A-54

Query Match 39.7%; Score 25; DB 1; Length 9;  
Best Local Similarity 57.1%; Pred. No. 3e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YGERFPD 8  
Db 2 FGSRFTD 8

RESULT 12  
US-08-278-091-23  
Sequence 23, Application US/08278091  
Patent No. 5506139  
GENERAL INFORMATION:  
APPLICANT: LOOSMORE, Sheena M  
APPLICANT: YANG, Yan-Ping  
APPLICANT: CHONG, Pele  
APPLICANT: COHEN, Raymond P.  
APPLICANT: KLEIN, Michel H.  
TITLE OF INVENTION: Analog of Haemophilus Hln47 Protein with  
REDUCED PROTEASE ACTIVITY  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sim & McBurney  
STREET: Suite 701, 330 University Avenue  
CITY: Toronto  
STATE: Ontario

COUNTRY: Canada  
ZIP: M5G 1R7  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/278,091  
FILING DATE: 21-JUL-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Stewart, Michael I.  
REGISTRATION NUMBER: 24,973  
REFERENCE/DOCKET NUMBER: 1038-371  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 595-1155  
TELEFAX: (416) 595-1163  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-278-091-23

Query Match 39.7%; Score 25; DB 1; Length 11;  
Best Local Similarity 37.5%; Pred. No. 3.1e+02;  
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGERPPDE 9  
DB 4 FGDRFAEQ 11

RESULT 13  
US-08-483-859-23  
Sequence 23, Application US/08483859  
Patent No. 5656436  
GENERAL INFORMATION:  
APPLICANT: LOOSMORE, Sheena M.  
APPLICANT: YANG, Yan-Ping  
APPLICANT: CHONG, Pele  
APPLICANT: COMEN, Raymond P.  
APPLICANT: KLEIN, Michel H.  
TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sim & McBurney  
STREET: Suite 701, 330 University Avenue  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5G 1R7  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,859  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/296,149  
FILING DATE: 26-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/278,091  
FILING DATE: 21-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Stewart, Michael I.  
REGISTRATION NUMBER: 24,973

REFERENCE/DOCKET NUMBER: 1038-495 MIS:Vg  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 595-1155  
TELEFAX: (416) 595-1163  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-483-859-23

Query Match 39.7%; Score 25; DB 1; Length 11;  
Best Local Similarity 37.5%; Pred. No. 3.1e+02;  
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGERPPDE 9  
DB 4 FGDRFAEQ 11

RESULT 14  
US-08-472-173-23  
Sequence 23, Application US/08472173  
Patent No. 5665353  
GENERAL INFORMATION:  
APPLICANT: LOOSMORE, Sheena M.  
APPLICANT: YANG, Yan-Ping  
APPLICANT: CHONG, Pele  
APPLICANT: COMEN, Raymond P.  
APPLICANT: KLEIN, Michel H.  
TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sim & McBurney  
STREET: Suite 701, 330 University Avenue  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5G 1R7  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/472,173  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/296,149  
FILING DATE: 26-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/278,091  
FILING DATE: 21-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Stewart, Michael I.  
REGISTRATION NUMBER: 24,973  
REFERENCE/DOCKET NUMBER: 1038-493 MIS:Vg  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 595-1155  
TELEFAX: (416) 595-1163  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-472-173-23

Query Match 39.7%; Score 25; DB 1; Length 11;  
Best Local Similarity 37.5%; Pred. No. 3.1e+02;



Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGERPPDE 9  
Db 4 FGDRFAEQ 11

RESULT 15

US-08-487-167-23  
Sequence 23, Application US/08487167  
Patent No. 3869302  
GENERAL INFORMATION:  
APPLICANT: LOOSMORE, Sheena M.  
APPLICANT: YANG, Yan-Ping  
APPLICANT: CHONG, Pele  
APPLICANT: COHEN, Raymond P.  
APPLICANT: KLEIN, Michel H.  
TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with  
REDUCED PROTEASE ACTIVITY  
NUMBER OF SEQUENCES: 23  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,167  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
TELEPHONE: (416) 595-1155  
TELEFAX: (416) 595-1155  
REGISTRATION NUMBER: 24,973  
REFERENCE/DOCKET NUMBER: 1038-508 MIS:V9  
TELECOMMUNICATION INFORMATION:  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-487-167-23

Query Match 39.7%; Score 25; DB 2; Length 11;  
Best Local Similarity 37.5%; Pred. No. 3.1e+02;  
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGERPPDE 9  
Db 4 FGDRFAEQ 11

RESULT 16  
US-08-482-816-23  
Sequence 23, Application US/08482816  
Patent No. 5935573  
GENERAL INFORMATION:  
APPLICANT: LOOSMORE, Sheena M  
APPLICANT: YANG, Yan-Ping

APPLICANT: CHONG, Pele  
APPLICANT: COHEN, Raymond P.  
APPLICANT: KLEIN, Michel H.  
TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with Reduced Protease Act  
NUMBER OF SEQUENCES: 23  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,816  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
TELEPHONE: (416) 595-1155  
TELEFAX: (416) 595-1155  
REGISTRATION NUMBER: 24,973  
REFERENCE/DOCKET NUMBER: 1038-494 MIS:V9  
TELECOMMUNICATION INFORMATION:  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-482-816-23

Query Match 39.7%; Score 25; DB 2; Length 11;  
Best Local Similarity 37.5%; Pred. No. 3.1e+02;  
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGERPPDE 9  
Db 4 FGDRFAEQ 11

RESULT 17  
US-08-296-149-23  
Sequence 23, Application US/08296149  
Patent No. 5939297  
GENERAL INFORMATION:  
APPLICANT: LOOSMORE, Sheena M  
APPLICANT: YANG, Yan-Ping  
APPLICANT: CHONG, Pele  
APPLICANT: COHEN, Raymond P.  
APPLICANT: KLEIN, Michel H.  
TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with  
REDUCED PROTEASE ACTIVITY  
NUMBER OF SEQUENCES: 23  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/296,149  
FILING DATE: 26-AUG-1994  
CLASSIFICATION: 435  
TELEPHONE: (416) 595-1155  
TELEFAX: (416) 595-1155  
REGISTRATION NUMBER: 24,973  
REFERENCE/DOCKET NUMBER: 1038-494 MIS:V9  
TELECOMMUNICATION INFORMATION:  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-296-149-23

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/296,149  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Stewart, Michael I  
REGISTRATION NUMBER: 24,973  
REFERENCE/DOCKET NUMBER: 1038-390  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 595-1155  
TELEFAX: (416) 595-1163  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-296-149-23

Query Match 39.7%; Score 25; DB 2; Length 11;  
Best Local Similarity 37.5%; Pred. No. 3.1e+02;  
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Oy 2 YGERPDE 9  
:||||:  
Db 4 FGDRFAEQ 11

RESULT 18  
US-08-801-499-23  
Sequence 23, Application US/08801499  
Patent No. 5962430  
GENERAL INFORMATION:  
APPLICANT: LOOSMORE, Sheena M  
APPLICANT: YANG, Yan-Ping  
APPLICANT: CHONG, Pele  
APPLICANT: COHEN, Raymond P.  
APPLICANT: KLEIN, Michel H.  
TITLE OF INVENTION: Analog of Haemophilus Hinf7 Protein with Reduced Protease Act  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Sim & McBurney  
STREET: 6th Floor, 330 University Avenue  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5G 1R7  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/801,499  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/482,816  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/296,149  
FILING DATE: 26-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/278,091  
FILING DATE: 21-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Stewart, Michael I  
REGISTRATION NUMBER: 24,973  
REFERENCE/DOCKET NUMBER: 1038-671 MTS:jb  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (416) 595-1155  
TELEFAX: (416) 595-1163  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-801-499-23

Query Match 39.7%; Score 25; DB 2; Length 11;  
Best Local Similarity 37.5%; Pred. No. 3.1e+02;  
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Oy 2 YGERPDE 9  
:||||:  
Db 4 FGDRFAEQ 11

RESULT 19  
US-08-615-271-23  
Sequence 23, Application US/08615271  
Patent No. 5981503  
GENERAL INFORMATION:  
APPLICANT: LOOSMORE, Sheena M.  
APPLICANT: YANG, Yan-Ping  
APPLICANT: CHONG, Pele  
APPLICANT: COHEN, Raymond P.  
APPLICANT: KLEIN, Michel H.  
TITLE OF INVENTION: ANALOG OF HAEMOPHILUS HINF7 WITH REDUCED  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Sim & McBurney  
STREET: 6th Floor, 330 University Avenue  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5G 1R7  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/615,271  
FILING DATE: 20-JUN-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Stewart, Michael I  
REGISTRATION NUMBER: 24,973  
REFERENCE/DOCKET NUMBER: 1038-580  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 595-1155  
TELEFAX: (416) 595-1163  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-615-271-23

Query Match 39.7%; Score 25; DB 2; Length 11;  
Best Local Similarity 37.5%; Pred. No. 3.1e+02;  
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Oy 2 YGERPDE 9  
:||||:  
Db 4 FGDRFAEQ 11

RESULT 20

US-09-074-660-23  
Sequence 23, Application US/09074660  
Patent No. 6020183  
GENERAL INFORMATION:  
APPLICANT: LOOSMORE, Sheena M.  
APPLICANT: YANG, Yan-Ping  
APPLICANT: CHONG, Pele  
APPLICANT: COMEN, Raymond P.  
APPLICANT: KLEIN, Michael H.  
TITLE OF INVENTION: Analog of Haemophilus HIN47 Protein with  
REDUCED PROTEASE ACTIVITY  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sim & McBurney  
STREET: 6th Floor, 330 University Avenue  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5G 1R7  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/074,660  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/487,167  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/296,149  
FILING DATE: 26-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/278,091  
FILING DATE: 21-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Stewart, Michael I.  
REGISTRATION NUMBER: 24,973  
REFERENCE/DOCKET NUMBER: 1038-731 MIS:jb  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 595-1155  
TELEFAX: (416) 595-1163  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-074-660-23

Query Match 39.7%; Score 25; DB 3; Length 11;  
Best Local Similarity 37.5%; Pred. No. 3.1e+02;  
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 YGERFPDE 9  
:|:|:|:  
Db 4 FGDRFAEQ 11

RESULT 21  
US-09-074-659-23  
Sequence 23, Application US/09074659  
Patent No. 6025342  
GENERAL INFORMATION:  
APPLICANT: LOOSMORE, Sheena M.  
APPLICANT: YANG, Yan-Ping  
APPLICANT: CHONG, Pele  
APPLICANT: COMEN, Raymond P.  
APPLICANT: KLEIN, Michael H.  
TITLE OF INVENTION: Analog of Haemophilus HIN47 Protein with  
REDUCED PROTEASE ACTIVITY  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sim & McBurney  
STREET: 6th Floor, 330 University Avenue  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5G 1R7  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sim & McBurney  
STREET: 6th Floor, 330 University Avenue  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5G 1R7  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/074,659  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/487,167  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/296,149  
FILING DATE: 26-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/278,091  
FILING DATE: 21-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Stewart, Michael I.  
REGISTRATION NUMBER: 24,973  
REFERENCE/DOCKET NUMBER: 1038-730 MIS:jb  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 595-1155  
TELEFAX: (416) 595-1163  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-074-659-23

Query Match 39.7%; Score 25; DB 3; Length 11;  
Best Local Similarity 37.5%; Pred. No. 3.1e+02;  
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 YGERFPDE 9  
:|:|:|:  
Db 4 FGDRFAEQ 11

RESULT 22  
US-09-106-468-23  
Sequence 23, Application US/09106468  
Patent No. 6114125  
GENERAL INFORMATION:  
APPLICANT: LOOSMORE, Sheena M.  
APPLICANT: YANG, Yan-Ping  
APPLICANT: CHONG, Pele  
APPLICANT: COMEN, Raymond P.  
APPLICANT: KLEIN, Michael H.  
TITLE OF INVENTION: ANALOG OF HAEMOPHILUS HIN47 WITH REDUCED  
PROTEASE ACTIVITY  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sim & McBurney  
STREET: 6th Floor, 330 University Avenue  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5G 1R7  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/106,468  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/615,271  
FILING DATE: 20-JUN-1996  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Stewart, Michael I  
REGISTRATION NUMBER: 24,973  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 595-1155  
TELEFAX: (416) 595-1163  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-106-468-23

Query Match 39.7%; Score 25; DB 3; Length 11;  
Best Local Similarity 37.5%; Pred. No. 3.1e+02;  
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGERFPDE 9  
DB 4 FGDRFAEQ 11

RESULT 23  
US-09-106-466A-23  
Sequence 23, Application US/09106466A  
Patent No. 6147057  
GENERAL INFORMATION:  
APPLICANT: LOOSMORE, Sheena M.  
APPLICANT: CHONG, Yan-Ping  
APPLICANT: COHEN, Raymond P.  
APPLICANT: KLEIN, Michael H.  
TITLE OF INVENTION: ANALOG OF HAEMOPHILUS HIN47 WITH REDUCED  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sim & McBurney  
STREET: 6th Floor, 330 University Avenue  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5G 1R7  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/106,466A  
FILING DATE:  
CLASSIFICATION: 514514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/615,271  
FILING DATE: 20-JUN-1996  
CLASSIFICATION: 514514  
ATTORNEY/AGENT INFORMATION:  
NAME: Stewart, Michael I  
REGISTRATION NUMBER: 24,973  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 595-1155  
TELEFAX: (416) 595-1163  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-106-467-23

TELEFAX: (416) 595-1163  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-106-466A-23

Query Match 39.7%; Score 25; DB 3; Length 11;  
Best Local Similarity 37.5%; Pred. No. 3.1e+02;  
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGERFPDE 9  
DB 4 FGDRFAEQ 11

RESULT 24  
US-09-106-467-23  
Sequence 23, Application US/09106467  
Patent No. 6153580  
GENERAL INFORMATION:  
APPLICANT: LOOSMORE, Sheena M.  
APPLICANT: CHONG, Yan-Ping  
APPLICANT: COHEN, Raymond P.  
APPLICANT: KLEIN, Michael H.  
TITLE OF INVENTION: ANALOG OF HAEMOPHILUS HIN47 WITH REDUCED  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sim & McBurney  
STREET: 6th Floor, 330 University Avenue  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5G 1R7  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/106,467  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/615,271  
FILING DATE: 20-JUN-1996  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Stewart, Michael I  
REGISTRATION NUMBER: 24,973  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 595-1155  
TELEFAX: (416) 595-1163  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-106-467-23

Query Match 39.7%; Score 25; DB 3; Length 11;  
Best Local Similarity 37.5%; Pred. No. 3.1e+02;  
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGERFPDE 9  
DB 4 FGDRFAEQ 11

RESULT 25  
US-08-945-168-95  
; Sequence 95, Application US/08945168  
; Patent No. 5989548  
; GENERAL INFORMATION:  
; APPLICANT: DILLNER, JOAKIM  
; TITLE OF INVENTION: PEPTIDE-BASED VACCINE AGAINST PAPILLOMA  
; TITLE OF INVENTION: VIRUS  
; NUMBER OF SEQUENCES: 117  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/945,168  
; FILING DATE: 18-DEC-1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/SE96/00533  
; FILING DATE: 23-APR-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: SE 9501512-9  
; FILING DATE: 24-APR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OBLON, NORMAN F.  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 7752-0002-0 PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-413-3000  
; TELEFAX: 703-413-2220  
; INFORMATION FOR SEQ ID NO: 95:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-945-168-95

Query Match 39.7%; Score 25; DB 2; Length 13;  
Best Local Similarity 57.1%; Pred. No. 3.7e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 3 GERPDE 9  
DB 3 GENVPDD 9  
RESULT 26  
US-08-999-689A-9  
; Sequence 9, Application US/08999689A  
; Patent No. 6541615  
; GENERAL INFORMATION:  
; APPLICANT: ULARICH, ALEX  
; APPLICANT: KHARITONENKOV, ALEXEI  
; APPLICANT: CHEN, ZHENGJUN  
; TITLE OF INVENTION: SIRP PROTEINS AND USES THEREOF  
; FILE REFERENCE: 038602/0548  
; CURRENT APPLICATION NUMBER: US/08/999,689A  
; FILING DATE: 1997-11-14  
; PRIOR APPLICATION NUMBER: 60/030,964  
; PRIOR FILING DATE: 1996-11-15

NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Rattus sp.  
US-08-999-689A-9

Query Match 39.7%; Score 25; DB 4; Length 13;  
Best Local Similarity 71.4%; Pred. No. 3.7e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 IYGERP 7  
DB 6 IGERHP 12

RESULT 27  
US-08-945-168-94  
; Sequence 94, Application US/08945168  
; Patent No. 5989548  
; GENERAL INFORMATION:  
; APPLICANT: DILLNER, JOAKIM  
; TITLE OF INVENTION: PEPTIDE-BASED VACCINE AGAINST PAPILLOMA  
; TITLE OF INVENTION: VIRUS  
; NUMBER OF SEQUENCES: 117  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/945,168  
; FILING DATE: 18-DEC-1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/SE96/00533  
; FILING DATE: 23-APR-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: SE 9501512-9  
; FILING DATE: 24-APR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OBLON, NORMAN F.  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 7752-0002-0 PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-413-3000  
; TELEFAX: 703-413-2220  
; INFORMATION FOR SEQ ID NO: 94:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-945-168-94

Query Match 39.7%; Score 25; DB 2; Length 14;  
Best Local Similarity 57.1%; Pred. No. 4e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 3 GERPDE 9  
DB 4 GENVPDD 10

## RESULT 28

US-07-861-458C-115  
Sequence 115, Application US/07861458C  
Patent No. 6232061  
GENERAL INFORMATION:  
APPLICANT: Marchionni, Mark Andrew  
APPLICANT: Johnson, Carl D.  
TITLE OF INVENTION: HOMOLOGY CLONING  
NUMBER OF SEQUENCES: 142  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 502 or 555X  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/861,458C  
FILING DATE: 04/01/92  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 04585/014001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 115:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8  
TYPE: amino acid  
TOPOLOGY: linear  
US-07-861-458C-115

Query Match 38.1%; Score 24; DB 3; Length 8;  
Best Local Similarity 57.1%; Pred. NO. 3e+05; 2; Indels 0; Gaps 0;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YGERFPD 8  
DB 1 YGDCVPD 7

## RESULT 29

US-08-569-166-23  
Sequence 23, Application US/08569166  
Patent No. 5830722  
GENERAL INFORMATION:  
APPLICANT: NICOLAS, LUC  
APPLICANT: CHARLES, JEAN-FRANCOIS  
APPLICANT: DEBECLOSE, ARYELLE  
APPLICANT: BARLOY, FREDERIQUE  
TITLE OF INVENTION: CLOSTRIDIUM BIPERMENTANS DNA FRAGMENT  
TITLE OF INVENTION: BEARING GENES CODING FOR PROTEINS LINKED TO AN  
TITLE OF INVENTION: INSECTICIDAL ACTIVITY  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
ADDRESS: P.C.  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA

## ZIP: 22202

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/569,166  
FILING DATE: 05-JUL-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR94/00768  
FILING DATE: 24-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 93/07795  
FILING DATE: 25-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 660-106-0 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-2220  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: amino acids  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-569-166-23

Query Match 38.1%; Score 24; DB 2; Length 9;  
Best Local Similarity 75.0%; Pred. NO. 3e+05; 0; Indels 2; Gaps 1;  
Matches 6; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 IYGERFPD 8  
DB 4 IYGE--PD 9

## RESULT 30

US-08-522-269B-6  
Sequence 6, Application US/08522269B  
Patent No. 5919690  
GENERAL INFORMATION:  
APPLICANT: Knapp, Inge Helmer  
APPLICANT: Hjort, Carsten W.  
APPLICANT: Halkier, Torben  
APPLICANT: Kolod, Lene Venke  
TITLE OF INVENTION: An Alpha-Galactosidase Enzyme  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 5919690 of No. 5919690th America, Inc.  
STREET: 405 Lexington Avenue, Suite 6400  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10174-6401  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/522,269B  
FILING DATE: 12-SEP-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Gregg, Valenta A.  
REGISTRATION NUMBER: 37,125  
REFERENCE/DOCKET NUMBER: 3935,204-US  
TELECOMMUNICATION INFORMATION:

Thu Sep 2 07:41:40 2004

us-09-720-469a-6.aug30.ra1

Page 13

TELEPHONE: 212 867 0123  
TELEFAX: 212 867 0298  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-522-2698-6

Query Match 38.1%; Score 24; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RFPD 8  
DB 3 RFPD 6

RESULT 31  
US-09-294-923-6  
Sequence 6, Application US/09294923  
Patent No. 6197566  
GENERAL INFORMATION:  
APPLICANT: Knap, Inge Helmer  
APPLICANT: Hjort, Carsten M.  
APPLICANT: Halkier, Jorden  
APPLICANT: Kotod, Lene Venke  
TITLE OF INVENTION: An Alpha-Galactosidase Enzyme  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: No. 6197566disk of No. 6197566th America, Inc.  
STREET: 405 Lexington Avenue, Suite 6400  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10174-6401  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/294,923  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/522,269  
FILING DATE: 12-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Gregg, Valeta A.  
REGISTRATION NUMBER: 37,125  
REFERENCE/DOCKET NUMBER: 3935,204-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212 867 0123  
TELEFAX: 212 867 0298  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-294-923-6

Query Match 38.1%; Score 24; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 RFPD 8  
DB 3 RFPD 6

RESULT 32  
US-08-960-780-59  
Sequence 59, Application US/08960780  
Patent No. 6204435  
GENERAL INFORMATION:  
APPLICANT: Feltelson, Gerald S.  
APPLICANT: Schneck, H. Ernest  
APPLICANT: Narva, Kenneth E.  
APPLICANT: Stockhoff, Brian A.  
APPLICANT: Schmeltz, James  
APPLICANT: Loewer, David  
APPLICANT: Dillum, Charles Joseph  
APPLICANT: Muller-Conn, Rudy  
APPLICANT: Stamp, Lisa  
TITLE OF INVENTION: No. 6204435el Pesticidal Toxins and Nucleotide  
NUMBER OF SEQUENCES: 134  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: FL  
COUNTRY: US  
ZIP: 32606-6669  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/960,780  
FILING DATE: 30-OCT-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/029,848  
FILING DATE: 30-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Saliwanchik, David R.  
REGISTRATION NUMBER: 31,794  
REFERENCE/DOCKET NUMBER: MA-708  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 352-375-8100  
TELEFAX: 352-372-5800  
INFORMATION FOR SEQ ID NO: 59:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-960-780-59

Query Match 38.1%; Score 24; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PDEN 10  
DB 1 PDEN 4

RESULT 33  
US-09-073-898-59  
Sequence 59, Application US/09073898  
Patent No. 6242669  
GENERAL INFORMATION:  
APPLICANT: Feltelson, Gerald S.  
APPLICANT: Schneck, H. Ernest  
APPLICANT: Narva, Kenneth E.  
APPLICANT: Stockhoff, Brian A.  
APPLICANT: Schmeltz, James

APPLICANT: Loewer, David  
APPLICANT: Dullum, Charles Joseph  
APPLICANT: Muller-Cohn, Judy  
APPLICANT: Stamp, Lisa  
APPLICANT: Morrill, George  
APPLICANT: Finstad-Lee, Stacey  
TITLE OF INVENTION: No. 624269e1 Pesticidal Toxins and Nucleotide  
NUMBER OF SEQUENCES: 144  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: FL  
COUNTRY: US  
ZIP: 32606-6669  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/073,898  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/029,848  
FILING DATE: 30-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/960,780  
FILING DATE: 30-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Sanders, Jay M.  
REGISTRATION NUMBER: 39,355  
REFERENCE/DOCKET NUMBER: MA-708C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 352-375-8100  
TELEFAX: 352-372-5800  
INFORMATION FOR SEQ ID NO: 59:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-073-898-59

Query Match 38.1%; Score 24; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PDEN 10  
DB 1 PDEN 4

RESULT 34  
US-09-518-046-65  
Sequence 65, Application US/09518046  
Patent No. 6294663  
GENERAL INFORMATION:  
APPLICANT: O'Brien, Timothy J.  
APPLICANT: Underwood, Lowell J.  
TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed  
TITLE OF INVENTION: in Ovarian Carcinoma and Uses Thereof  
FILE REFERENCE: D6192CIP  
CURRENT APPLICATION NUMBER: US/09/518,046  
CURRENT FILING DATE: 2000-03-02  
EARLIER APPLICATION NUMBER: 09/261,416  
EARLIER FILING DATE: 1999-03-03  
NUMBER OF SEQ ID NOS: 153  
SEQ ID NO 65  
LENGTH: 9

TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
LOCATION: 328...336  
OTHER INFORMATION: TADG-12 peptide  
US-09-518-046-65

Query Match 38.1%; Score 24; DB 3; Length 9;  
Best Local Similarity 80.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPD 8  
DB 4 ENFPD 8

RESULT 35  
US-09-518-046-79  
Sequence 79, Application US/09518046  
Patent No. 6294663  
GENERAL INFORMATION:  
APPLICANT: O'Brien, Timothy J.  
APPLICANT: Underwood, Lowell J.  
TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed  
TITLE OF INVENTION: in Ovarian Carcinoma and Uses Thereof  
FILE REFERENCE: D6192CIP  
CURRENT APPLICATION NUMBER: US/09/518,046  
CURRENT FILING DATE: 2000-03-02  
EARLIER APPLICATION NUMBER: 09/261,416  
EARLIER FILING DATE: 1999-03-03  
NUMBER OF SEQ ID NOS: 153  
SEQ ID NO 79  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
LOCATION: 329...337  
OTHER INFORMATION: TADG-12 peptide  
US-09-518-046-79

Query Match 38.1%; Score 24; DB 3; Length 9;  
Best Local Similarity 80.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPD 8  
DB 3 ENFPD 7

RESULT 36  
US-09-518-046-144  
Sequence 144, Application US/09518046  
Patent No. 6294663  
GENERAL INFORMATION:  
APPLICANT: O'Brien, Timothy J.  
APPLICANT: Underwood, Lowell J.  
TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed  
TITLE OF INVENTION: in Ovarian Carcinoma and Uses Thereof  
FILE REFERENCE: D6192CIP  
CURRENT APPLICATION NUMBER: US/09/518,046  
CURRENT FILING DATE: 2000-03-02  
EARLIER APPLICATION NUMBER: 09/261,416  
EARLIER FILING DATE: 1999-03-03  
NUMBER OF SEQ ID NOS: 153  
SEQ ID NO 144  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
LOCATION: 330...338  
OTHER INFORMATION: TADG-12 peptide  
US-09-518-046-144



Query Match 38.1%; Score 24; DB 3; Length 9;  
Best Local Similarity 80.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPD 8  
|  
|  
|  
|  
Db 2 ENFPD 6

RESULT 37  
US-09-618-259-51  
; Sequence 51, Application US/09618259  
; Patent No. 6642013  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, Timothy J.  
; APPLICANT: Underwood, Lowell J.  
; TITLE OF INVENTION: No. 6642013el Extracellular Serine Protease  
; FILE REFERENCE: D6020CIP2  
; CURRENT FILING DATE: US/09/618,259  
; PRIOR FILING DATE: 2000-07-18  
; PRIOR APPLICATION NUMBER: US 09/127,444  
; NUMBER OF SEQ ID NOS: 72  
; SEQ ID NO 51  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Residues 162-170 of the TADG-14 protein  
US-09-618-259-51

Query Match 38.1%; Score 24; DB 4; Length 9;  
Best Local Similarity 80.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPD 8  
|  
|  
|  
|  
Db 4 ENFPD 8

RESULT 38  
US-09-618-259-70  
; Sequence 70, Application US/09618259  
; Patent No. 6642013  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, Timothy J.  
; APPLICANT: Underwood, Lowell J.  
; TITLE OF INVENTION: No. 6642013el Extracellular Serine Protease  
; FILE REFERENCE: D6020CIP2  
; CURRENT FILING DATE: US/09/618,259  
; PRIOR FILING DATE: 2000-07-18  
; PRIOR APPLICATION NUMBER: US 09/127,444  
; NUMBER OF SEQ ID NOS: 72  
; SEQ ID NO 70  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Residues 164-172 of the TADG-14 protein  
US-09-618-259-70

Query Match 38.1%; Score 24; DB 4; Length 9;  
Best Local Similarity 80.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPD 8  
|  
|  
|  
|  
Db 2 ENFPD 6

RESULT 39  
US-09-850-351A-59

; Sequence 59, Application US/09850351A  
; Patent No. 6656908  
; GENERAL INFORMATION:  
; APPLICANT: Feltelson, Gerald S.  
; Schnepf, H. Ernest  
; Narva, Kenneth E.  
; Stockhoff, Brian A.  
; Schmeits, James  
; Loewer, David  
; Dullum, Charles Joseph  
; Muller-Cohn, Judy  
; Stamp, Lisa  
; Mortill, George

TITLE OF INVENTION: No. 6656908el Pesticidal Toxins and Nucleotide  
Sequences which Encode These Toxins

NUMBER OF SEQUENCES: 144  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Saliwanchik, Lloyd & Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: FL  
COUNTRY: US  
ZIP: 32606-6669

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/850,351A  
FILING DATE: 07-May-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/073,898  
FILING DATE: 06-May-1998

APPLICATION NUMBER: US 08/960,780  
FILING DATE: 30-OCT-1997

APPLICATION NUMBER: US 60/029,848  
FILING DATE: 30-OCT-1996

ATTORNEY/AGENT INFORMATION:  
NAME: Sanders, Jay M.  
REGISTRATION NUMBER: 39,355  
REFERENCE/DOCKET NUMBER: MA-708CD1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 352-375-8100  
TELEFAX: 352-372-5800

INFORMATION FOR SEQ ID NO: 59:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 59:  
US-09-850-351A-59

Query Match 38.1%; Score 24; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PDEN 10  
|  
|  
|  
|  
Db 1 PDEN 4

RESULT 40  
US-08-151-574-3  
; Sequence 3, Application US/08151574  
; Patent No. 5436156  
; GENERAL INFORMATION:  
; APPLICANT: Robert F.M. Van Gorcom  
; APPLICANT: Willem Van Hartingsveldt  
; APPLICANT: Petrus A. Van Paridon

APPLICANT: Annemarie E. Veenstra  
APPLICANT: Rudolf G.M. Luttin  
APPLICANT: Gerardus Seltien  
TITLE OF INVENTION: Cloning and Expression of Microbial  
TITLE OF INVENTION: Phytase  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster  
STREET: 545 Middlefield Road, Suite 200  
CITY: Menlo Park  
STATE: California  
COUNTRY: USA  
ZIP: 94025-3471  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.25  
SOFTWARE:  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/151,574  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/688,578  
FILING DATE: 24-MAY-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 24615-20026.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-327-7250  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHEtical: NO  
FRAGMENT TYPE: N-terminal  
US-08-151-574-3

Query Match 38.1%; Score 24; DB 1; Length 10;  
Best Local Similarity 57.1%; Pred. No. 4.2e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
CY 1 YGERFP 7  
DB 1 VYDERFP 7  
RESULT 41  
US-08-300-386A-59  
Sequence 59, Application US/08300386A  
Patent No. 5667988  
GENERAL INFORMATION:  
APPLICANT: Barbas, Carlos F. III  
APPLICANT: Burton, Dennis R.  
APPLICANT: Lerner, Richard A.  
TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES  
TITLE OF INVENTION: USING UNIVERSAL OR RANDOMIZED IMMUNOGLOBULIN LIGHT CHAINS  
NUMBER OF SEQUENCES: 70  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: The Scripps Research Institute  
STREET: 10666 No. 5667988th Torrey Pines Road, TPC8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/300,386A  
FILING DATE: 02-SEP-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/174,674  
FILING DATE: 28-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/826,623  
FILING DATE: 27-JAN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/954,148  
FILING DATE: 30-SEP-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/012,566  
FILING DATE: 02-FEB-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSRI 409.1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2937  
TELEFAX: 619-554-6312  
INFORMATION FOR SEQ ID NO: 59:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-300-386A-59

Query Match 38.1%; Score 24; DB 1; Length 10;  
Best Local Similarity 66.7%; Pred. No. 4.2e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
CY 2 YGERFP 7  
DB 3 YKRRSP 8  
RESULT 42  
US-08-419-448-3  
Sequence 3, Application US/08419448  
Patent No. 5863533  
GENERAL INFORMATION:  
APPLICANT: Robert F.M. Van Gorkom  
APPLICANT: Willem Van Hattingsveldt  
APPLICANT: Petrus A. Van Paridon  
APPLICANT: Annemarie E. Veenstra  
APPLICANT: Rudolf G.M. Luttin  
TITLE OF INVENTION: Cloning and Expression of Microbial  
TITLE OF INVENTION: Phytase  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster  
STREET: 2000 Pennsylvania Ave. N.W., Suite 5500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20006-1888  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/419,448  
FILING DATE: 10-APR-1995  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 24615-20026.10  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-887-1500  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHEICAL: NO  
FRAGMENT TYPE: N-terminal  
US-08-419-448-3

Query Match 38.1%; Score 24; DB 2; Length 10;  
Best Local Similarity 57.1%; Pred. No. 4.2e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Cy 1 YGERFP 7  
Db 1 VDERFP 7

## RESULT 43

US-08-931-645-59  
Sequence 59, Application US/08931645

GENERAL INFORMATION:  
APPLICANT: Barbas, Carlos F, III  
APPLICANT: Burton, Dennis R  
APPLICANT: Lerner, Richard A  
TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES  
TITLE OF INVENTION: USING UNIVERSAL OR RANDOMIZED IMMUNOGLOBULIN LIGHT CHAINS  
NUMBER OF SEQUENCES: 70  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: The Scripps Research Institute  
STREET: 10666 No. 6096551th Torrey Pines Road, TPC8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/931,645  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/300,386  
FILING DATE: 02-SEP-1994  
APPLICATION NUMBER: US 08/174,674  
FILING DATE: 28-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/826,623  
FILING DATE: 27-JAN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/954,148  
FILING DATE: 30-SEP-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/012,566  
FILING DATE: 02-FEB-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSRI 409.1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2937  
TELEFAX: 619-554-6312

INFORMATION FOR SEQ ID NO: 59:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-931-645-59

Query Match 38.1%; Score 24; DB 3; Length 10;  
Best Local Similarity 66.7%; Pred. No. 4.2e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Cy 2 YGERFP 7  
Db 3 YGRSP 8

## RESULT 44

US-09-233-510-3  
Sequence 3, Application US/09233510

GENERAL INFORMATION:  
APPLICANT: Robert F.M. Van Gorcom  
APPLICANT: Willem Van Hartingsveldt  
APPLICANT: Petrus A. Van Paridon  
APPLICANT: Annemarie E. Veenstra  
APPLICANT: Rudolf G.M. Luttin  
TITLE OF INVENTION: Cloning and Expression of Microbial  
TITLE OF INVENTION: Phytase  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster  
STREET: 545 Middlefield Road, Suite 200  
CITY: Menlo Park  
STATE: California  
COUNTRY: USA  
ZIP: 94025-3471  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/233,510  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/688,578  
FILING DATE: 24-MAY-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 24615-20026.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-327-7250  
TELEFAX: 415-327-2951  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHEICAL: NO  
FRAGMENT TYPE: N-terminal  
US-09-233-510-3

Query Match 38.1%; Score 24; DB 4; Length 10;  
Best Local Similarity 57.1%; Pred. No. 4.2e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 IYGERFP 7  
: |||  
Db 1 VYDERFP 7

## RESULT 45

PCT-US93-08067-4  
; Sequence 4, Application PC/TUS9308067  
; GENERAL INFORMATION:  
; APPLICANT: Silva, Robert F  
; APPLICANT: Reilly, John D  
; TITLE OF INVENTION: PORTABLE INTRON AS AN INSERTION VECTOR FOR  
; TITLE OF INVENTION: GENE INSERTION  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jacobson, Price, Holman & Stern  
; STREET: 400 Seventh St. N.W.  
; CITY: Washington D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20004-2201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/08067  
; FILING DATE: 27-AUG-1993  
; CLASSIFICATION:  
; CLASSIFICATION: 435/235  
; CLASSIFICATION: C12N 7/00  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: U.S. Application No. 07/936,423  
; FILING DATE: 27-AUG-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Holman, John C.  
; REGISTRATION NUMBER: 22,769  
; REFERENCE/DOCKET NUMBER: 043813PC  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 638-6666  
; TELEFAX: (202) 393-5350  
; TELEEX: RCA 248593 IDBA UR  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; PCT-US93-08067-4

Query Match 38.1%; Score 24; DB 5; Length 10;  
Best Local Similarity 50.0%; Pred. No. 4.2e+02;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 6 PPDENF 11  
: |||  
Db 4 YPDNPF 9

Search completed: August 30, 2004, 10:57:16  
Job time : 5.34797 secs

Thu Sep 2 07:41:39 2004

us-09-720-469a-6.aug30.1.aag

Page 1

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:39:14 ; Search time 16.3885 Seconds  
(without alignments)  
189.646 Million cell updates/sec

Title: US-09-720-469a-6  
Perfect score: 63 IYGERPPDENF 11  
Sequence: 1 IYGERPPDENF 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 309569

Minimum DB seq length: 8  
Maximum DB seq length: 14

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq 29Jan04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63	100.0	11	3	AAV69926 Human cyc
2	41	65.1	9	3	AAV69927 Human cyc
3	31	49.2	10	7	ADA06843 Solid-pha
4	30	47.6	10	2	AAW44362 Breast ca
5	30	47.6	10	4	AAW98714 Human bre
6	30	47.6	13	7	ADD23953 Breast ca
7	29	46.0	10	2	ADC21550 Human col
8	29	46.0	12	2	AAW07435 HSV-1 TK
9	29	46.0	12	4	AAW97167 S. chryso
10	29	46.0	12	4	AAW85216 S. chryso
11	29	46.0	12	5	ABG99226 Thymidine
12	28	44.4	9	4	AD43381 Variola s
13	28	44.4	9	4	AAU68482 Human Bre
14	28	44.4	9	4	AAU68482 Clone 2 s
15	28	44.4	9	5	ABG67487 Human ADP
16	28	44.4	9	6	ABR58800 Alzheim
17	28	44.4	9	6	ADA23600 Alzheim
18	28	44.4	9	7	ABR62869 Tumourige
19	28	44.4	9	7	AD43382 Variola s
20	28	44.4	9	7	AD43385 Variola s
21	28	44.4	10	7	AD43396 Variola s
22	28	44.4	10	7	AD43409 Variola s
23	28	44.4	10	7	AD43383 Variola s
24	28	44.4	11	7	AD43397 Variola s
25	28	44.4	11	7	AD43410 Variola s

26	28	44.4	11	7	ADC43384	ADC43384 Variola s
27	28	44.4	11	7	ADC43422	ADC43422 Variola s
28	28	44.4	12	7	ADC43411	ADC43411 Variola s
29	28	44.4	12	7	ADC43385	ADC43385 Variola s
30	28	44.4	12	7	ADC43423	ADC43423 Variola s
31	28	44.4	12	7	ADC43434	ADC43434 Variola s
32	28	44.4	12	7	ADC43398	ADC43398 Variola s
33	28	44.4	12	7	ADC43403	ADC43403 Endotheli
34	28	44.4	12	7	ADC36084	ADC36084 Chemokine
35	28	44.4	13	2	AAW46829	AAW46829 PH 2.5 ac
36	28	44.4	13	2	ADC43445	ADC43445 Variola s
37	28	44.4	13	7	ADC43424	ADC43424 Variola s
38	28	44.4	13	7	ADC43399	ADC43399 Variola s
39	28	44.4	13	7	ADC43412	ADC43412 Variola s
40	28	44.4	13	7	ADC43435	ADC43435 Variola s
41	28	44.4	13	7	ADC43386	ADC43386 Variola s
42	28	44.4	14	7	ADC43436	ADC43436 Variola s
43	28	44.4	14	7	ADC43387	ADC43387 Variola s
44	28	44.4	14	7	ADC43413	ADC43413 Variola s
45	28	44.4	14	7	ADC43425	ADC43425 Variola s

## ALIGNMENTS

RESULT 1  
ID AAV69926 standard; peptide; 11 AA.

AAV69926; 11-APR-2000 (first entry)

Human cyclophilin B peptide fragment #6.

Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL; HLA antigen; diagnosis; tumour; therapy.

OS Homo sapiens.

XX NO9967288-A1.

XX 29-DEC-1999.

XX 24-JUN-1999; 99WO-JP003360.

XX 25-JUN-1998; 98JP-00178449.

XX (SUMU) SUMITOMO PHARM CO LTD.  
(ITOH/) ITOH K.

XX Itoh K, Gomi S;

XX WPI; 2000-116932/10.

XX Tumor antigen peptides derived from cyclophilin B for treatment and diagnosis of tumors.

XX Claim 4; Page 50; 64pp; Japanese.

XX This sequence represents a cyclophilin B peptide of the invention. The peptides are tumour antigen peptides derived from cyclophilin B, that recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The peptides are used for the treatment and diagnosis of tumours

XX Sequence 11 AA;

Query Match 100.0%; Score 63; DB 3; Length 11;  
Best local similarity 100.0%; Pred. No. 0.00025;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IYGERPPDENF 11  
|||||

Db 1 TYGERPPDENF 11

RESULT 2  
AAV69927  
ID AAV69927 standard; peptide; 9 AA.  
XX  
AC AAV69927;  
XX  
DT 11-APR-2000 (first entry)  
XX  
DE Human cyclophilin B peptide fragment #7.  
XX  
KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;  
XX HLA antigen; diagnosis; tumour; therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO967288-A1.  
XX  
PD 29-DEC-1999.  
XX  
PF 24-JUN-1999; 99WO-JP003360.  
XX  
PR 25-JUN-1998; 98JP-00178449.  
XX  
PA (SUMU) SUMITOMO PHARM CO LTD.  
XX (ITOH) ITOH K.  
XX  
PI Itoh K, Gomi S;  
XX  
DR WPI; 2000-116932/10.  
XX  
PT Tumour antigen peptides derived from cyclophilin B for treatment and  
XX diagnosis of tumors.  
XX  
PS Claim 4; Page 51; 64pp; Japanese.  
XX  
CC This sequence represents a cyclophilin B peptide of the invention. The  
CC peptides are tumour antigen peptides derived from cyclophilin B, that  
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The  
CC peptides are used for the treatment and diagnosis of tumours  
XX  
SQ Sequence 9 AA;  
XX

Query Match 65.1%; Score 41; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RFPDENF 11  
Db 1 RFPDENF 7

RESULT 3  
ADA06843  
ID ADA06843 standard; peptide; 10 AA.  
XX  
AC ADA06843;  
XX  
DT 06-MAY-2003 (first entry)  
XX  
DE Solid-phase synthesis produced organic peptide #5.  
XX  
KW Aldehyde functionalised support material; solid-phase synthesis;  
XX organic compound; acid; thioacid; thioester; alcohol;  
XX disubstituted amide; aldehyde.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1  
PT /label= OTHER

FT /note= "OTHER= "Fmoc-Arg"  
FT Misc-difference 2  
FT /note= "D-form residue"  
FT Modified-site 10  
FT /label= OTHER  
FT /note= "OTHER= "Ala-OAl"  
XX  
XX US566494-B1.  
XX  
XX 20-MAY-2003.  
XX  
XX  
XX 11-MAY-1999; 99US-00309828.  
XX  
XX 18-JUN-1996; 96US-00665509.  
XX  
XX (MINU) UNIV MINNESOTA.  
XX  
XX Jensen KJ, Barany G, Songster MF, Albericio F, Alsina J;  
XX Vagner J;  
XX  
XX WPI; 2003-596202/56.  
XX  
XX New aldehyde functionalized support material used for solid phase organic  
XX synthesis.  
XX  
XX Example 14; Col 18; 18pp; English.  
XX  
XX The invention is related to an aldehyde functionalised support material.  
XX The aldehyde functionalised support material is used for solid-phase  
XX synthesis of organic compounds, particularly peptides. The organic  
XX compounds can have a variety of C-terminal functionalities e.g. acids,  
XX thioacids, thioesters, alcohols, disubstituted amides and aldehydes can  
XX be produced. This sequence represents an organic peptide prepared by  
XX solid-phase synthesis, using the support material of the invention.  
XX  
SQ Sequence 10 AA;  
XX

Query Match 49.2%; Score 31; DB 7; Length 10;  
Best Local Similarity 57.1%; Pred. No. 98;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 5 RFPDENF 11  
Db 1 RFPDENF 7

RESULT 4  
AAW44362  
ID AAW44362 standard; peptide; 10 AA.  
XX  
AC AAW44362;  
XX  
DT 28-MAY-1998 (first entry)  
XX  
DE Breast cancer-associated protein fragment BC-8 SEQ ID NO:8.  
XX  
KW Human; breast cancer-associated protein; nuclear matrix protein;  
XX detection; diagnosis; antibody.  
XX  
OS Homo sapiens.  
XX  
PN WO9746884-A1.  
XX  
PD 11-DEC-1997.  
XX  
PF 03-JUN-1997; 97WO-US009529.  
XX  
PR 05-JUN-1996; 96US-00658639.  
XX  
XX (MATR-) MATRITECH INC.  
XX  
XX Keesee SK, Obar R, Wu Y;  
XX

DR WPI; 1998-042336/04.

XX Diagnosing breast cancer by detecting a breast cancer-associated protein  
PT - allows early and reliable diagnosis and treatment monitoring, and  
PT antibody or inhibitory compounds useful for treating breast cancer.  
XX  
PS Claim 10; Page 30; 47pp; English.

XX The present sequence represents a breast cancer-associated protein  
CC fragment for use in a method for diagnosing breast cancer in tissue or  
CC body fluid by detecting one or more breast cancer-associated protein(s).  
CC Alternatively a nucleic acid encoding a breast cancer-associated protein  
CC is detected in the sample by the use of a nucleic acid probe. The breast  
CC cancer-associated proteins, encoding nucleic acids and antibodies are  
CC useful in diagnostic assays and kits for breast cancer detection. The  
CC proteins are also useful in screening for inhibitory compounds and  
CC monitoring effectiveness of treatments. The antibody, or pharmaceutical  
CC compositions containing the antibody or the inhibitory compound, can be  
CC administered to patients to treat breast cancer. The methods allow  
CC reliable and early diagnosis of breast cancer, or prediction of its  
CC onset, by detection of specific markers expressed in breast tumour cells  
CC but not in non-cancerous breast cells

XX Sequence 10 AA;

Query Match 47.6%; Score 30; DB 2; Length 10;  
Best Local Similarity 71.4%; Pred. No. 1.5e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 RFPDENF 11  
: |||||  
Db 1 KFDENF 7

RESULT 5  
AAB98714  
ID AAB98714 standard; peptide; 10 AA.

XX AAB98714;

XX 29-AUG-2001 (first entry)

DE Human breast cancer-associated protein BC-8 peptide, SEQ ID NO:8.

XX Human breast cancer-associated protein; BC-8; marker protein;

KW nuclear matrix protein; diagnosis; detection; tumour.

XX Homo sapiens.

XX US6218131-B1.

XX 17-APR-2001.

XX 06-OCT-1997; 97US-00944604.

XX 05-JUN-1996; 96US-00658639.

XX (MATR-) MATRITTECH INC.

XX Keesee SK, Obar R, Wu Y;

DR WPI; 2001-396355/42.

XX Diagnosing or detecting breast cancer in an individual comprises  
PT detecting the presence of breast cancer-associated proteins in a  
PT biological sample.

XX Claim 9; Col 8; 30pp; English.

XX The invention relates to novel human breast cancer-associated proteins,  
CC and their use in diagnosing and detecting breast cancer. The breast  
CC cancer-associated proteins of the invention are nuclear matrix proteins  
CC designated BC-2 (AAB98720), BC-8 isoform A (BC-8A, AAB98721) and CC BC-8

CC isoform B (BC-8B, AAB98722), although 6 other breast cancer-associated  
CC nuclear matrix proteins (BC-1, BC-3, BC-4, BC-5, BC-6, and BC-7) were  
CC also isolated (sequences not given in the specification). The novel  
CC breast cancer-associated proteins are present in the nuclear matrix of  
CC breast cancer cells, but are not present in the nuclear matrix of cells  
CC from normal breast tissue. The invention also encompasses fragments of  
CC the breast cancer-associated proteins (AAB98709-AAB98716), and methods  
CC for their use in breast cancer diagnosis. The breast cancer marker  
CC proteins of the invention or fragments thereof may be detected in a  
CC sample of breast tissue or blood from an individual. Isolated breast  
CC cancer-associated proteins may also be used to prepare antibodies,  
CC particularly monoclonal antibodies, which may be used to detect or  
CC diagnose breast cancer. Nucleic acids encoding the breast cancer-  
CC associated proteins may also be used in the diagnosis and detection of  
CC breast cancer, and in the isolation of DNA or protein sequences which may  
CC interact with breast cancer-associated nuclear matrix proteins. Sequences  
CC AAB98712-AAB98716 represent specifically claimed fragments of breast  
CC cancer-associated protein BC-8

XX Sequence 10 AA;

Query Match 47.6%; Score 30; DB 4; Length 10;  
Best Local Similarity 71.4%; Pred. No. 1.5e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 RFPDENF 11  
: |||||  
Db 1 KFDENF 7

RESULT 6  
ADD23953  
ID ADD23953 standard; peptide; 13 AA.

XX ADD23953;

XX 15-JAN-2004 (first entry).

DE Breast cancer membrane protein (BCMP) peptide SEQ ID NO:928.

XX breast cancer; screening; diagnosis; breast cancer therapy;

KW breast cancer membrane protein; BCMP; cytostatic; vaccine; human.

XX Homo sapiens.

XX WO2003087831-A2.

XX 23-OCT-2003.

XX 10-APR-2003; 2003WO-GB001559.

XX 11-APR-2002; 2002GB-00008331.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX Hudson LJ, Stamps AC, Terrett JA;

DR WPI; 2003-845381/78.

XX Screening, diagnosing and/or treating breast cancer by detecting a change  
PT in expression or activity of a breast cancer membrane protein (BCMP)  
PT polypeptide or encoding nucleic acid molecule.

XX Example; SEQ ID NO 928; 81pp; English.

XX The present invention describes a method of screening for and/or  
CC diagnosing breast cancer in a subject, and/or monitoring the  
CC effectiveness of breast cancer therapy. The method comprises detecting  
CC and/or quantifying in a biological sample obtained from the subject a  
CC breast cancer membrane protein (BCMP) polypeptide and a nucleic acid  
CC molecule. Also described: (1) an antibody, its functionally-active  
CC fragment, derivative or analogue, that specifically binds to one or more  
CC of the BCMP polypeptide; (2) a diagnostic kit comprising a capture

CC reagent specific for an BCPM polypeptide, reagents and instructions for  
 CC use; (3) a method for screening for anti-breast cancer agents that  
 CC interact with the BCPM polypeptide, comprising contacting the polypeptide  
 CC with a candidate agent, and determining whether or not the candidate  
 CC agent interacts with the polypeptide; (4) a method for screening for anti-  
 CC breast cancer agents that modulate the expression or activity of an BCPM  
 CC polypeptide or the nucleic acid molecule cited above, comprising  
 CC comparing the expression or activity of the polypeptide or nucleic acid  
 CC molecule, in the presence and absence of a candidate agent or in the  
 CC presence of a control agent, and determining whether the candidate agent  
 CC causes the expression or activity of the polypeptide or nucleic acid  
 CC molecule to change; and (5) an agent identified by the method of (3) or  
 CC (4), which interacts with the polypeptide or causes the expression or  
 CC activity of the polypeptide, or the expression of the nucleic acid  
 CC molecule to change. BCPMs have cytoskeletal activities, and can be used in  
 CC vaccines. The BCPM polypeptide, nucleic acid molecule, antibody, agent or  
 CC their derivatives, are useful in the manufacture of a vaccine for the  
 CC treatment of breast cancer, where the composition is a vaccine. The  
 CC present sequence represents a BCPM peptide which is used in the  
 CC exemplification of the present invention.

CC Sequence 13 AA;

Query Match 47.6%; Score 30; DB 7; Length 13;  
 Best Local Similarity 71.4%; Pred. No. 1.9e+02;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERPPDEN 10  
 Db 1 EEPFVEN 7

RESULT 7

ID ADC21550 standard; peptide; 10 AA.

AC ADC21550;

DT 18-DEC-2003 (first entry)

DE Human collagen II epitope peptide SeqID7.

XX triple helix formation sequence; interpolypeptide linkage;  
 KW rheumatoid arthritis; autoimmune disease; inflammatory disease;  
 KW peripheral joint; major histocompatibility complex class II region;  
 KW HLA-DR; T cell; joint specific antigen; B cell; type II collagen; CII;  
 KW antiarthritic; antirheumatic; immunosuppressive; dermatological;  
 KW antiinflammatory; antipsoriatic; antiasthmatic; neuoprotective;  
 KW relapsing polychondritis; systemic lupus erythematosus; psoriasis;  
 KW asthma; Sjogren's syndrome; multiple sclerosis; epitope peptide; human.

OS Homo sapiens.

PN WO2003006603-A2.

PD 23-JAN-2003.

XX 11-JUL-2002; 2002WO-IB004256.

PR 12-JUL-2001; 2001US-0305048P.

PA (AREX-) AREXIS AB.

PI Holmdahl R, Burkhardt H, Engstrom JA, Kinberg J;

DR WPI; 2003-221724/21.

PT Composition for treating autoimmune disorders such as rheumatoid  
 PT arthritis, comprises three polypeptides, each comprising a triple helix  
 PT formation sequence, and at least two interpolypeptide linkages.

PS Claim 17; SEQ ID NO 7; 113pp; English.

XX

CC This invention relates to a novel composition comprising three  
 CC polypeptides, where each polypeptide comprises a triple helix formation  
 CC sequence and at least two interpolypeptide linkages such that each  
 CC polypeptide is attached to at least one of the other two polypeptides.  
 CC Rheumatoid arthritis is an autoimmune, inflammatory disease that affects  
 CC peripheral joints. The main genetic association is to the major  
 CC histocompatibility complex class II region (HLA-DR), suggesting that T  
 CC cell mediated autoimmune recognition of joint specific antigens is  
 CC involved in the disease. In addition, B cell mediated autoimmune  
 CC responses have been observed in rheumatoid joints. Specifically, B cells  
 CC have been detected secreting IgG antibodies specific for type II collagen  
 CC (CII). The compounds of the invention may be antiarthritic,  
 CC antiinflammatory, immunosuppressive, dermatological, antiinflammatory,  
 CC antipsoriatic, antiasthmatic or vasoprotective through the enhancement of  
 CC tolerance to the endogenous polypeptide. The compounds may be useful for  
 CC diagnosing and treating autoimmune conditions such as rheumatoid  
 CC arthritis, relapsing polychondritis, systemic lupus erythematosus,  
 CC psoriasis, chronic stages of asthma, Jorger's syndrome and multiple  
 CC sclerosis. The present sequence is that of a human type II collagen (CII)  
 CC peptide epitope of the invention.

CC Sequence 10 AA;

Query Match 46.0%; Score 29; DB 7; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GERFP 7  
 Db 6 GERFP 10

RESULT 8

ID AA07435 standard; peptide; 12 AA.

AC AA07435;

DT 16-JUL-1999 (first entry)

DE HSV-1 TK amino acids 159-173 mutant #27.

XX HSV-1; thymidine kinase; mutation; DNA nucleoside binding site; enzyme;  
 KW pathogen; tumor; hyperkeratosis; psoriasis; prostate hypertrophy;  
 KW hyperthyroidism; endocrinopathy; autoimmune disease; allergy; restenosis;  
 KW viral disease; AIDS; hepatitis; parasite; bacterial infection.

OS Herpes simplex virus unknown type.

PN WO9919466-A2.

PD 22-APR-1999.

XX 14-OCT-1998; 98WO-US021672.

PR 14-OCT-1997; 97US-0061812P.

PA (DARW-) DARWIN MOLECULAR CORP.

PI Black ME;

DR WPI; 1999-277631/23.

PT New Herpesviridae thymidine kinase mutants - useful for treating prostate  
 PT hypertrophy, allergies, cystic fibrosis and Alzheimer's disease.

PS Disclosure; Fig 15; 126pp; English.  
 CC This sequence represents a mutant form of amino acids 159-173 of the  
 CC herpes simplex virus type 1 (HSV-1) thymidine kinase (TK) protein which  
 CC was used to generate mutant TK proteins. The invention relates to the  
 CC generation of novel HSV-1 TK or guanylate kinase (GK) genes with a





DE	Thymidine kinase (TK) residues 159-173 mutant #29.	
XX		
KM	Herpesviridae; thymidine kinase; TK; DRH nucleoside binding region;	
KM	viral inhibitor; bacterial inhibitor; parasite inhibitor; tumour;	
KM	autoreactive immune cell; cancer; hyperkeratosis; psoriasis;	
KM	prostate hypertrophy; hyperthyroidism; endocrinopathy; allergy;	
KM	autoimmune disease; retinosis; viral disease; AIDS; hepatitis; HCV; HBV;	
KM	acquired immunodeficiency syndrome; intracellular parasitic disease;	
KM	Gene therapy; adenosine deaminase deficiency; Alzheimer's disease;	
XX	mutant; muclein.	
OS	Herpesviridae.	
OS	Synthetic.	
XX		
PN	US6451571-B1.	
XX		
PD	17-SEP-2002.	
XX		
PF	17-MAR-1999; 99US-00270956.	
XX		
PR	02-MAY-1994; 94US-00237592.	
PR	02-MAY-1995; 95US-00432871.	
PR	02-NOV-1995; 95US-00552304.	
XX		
PA	(UNITM ) UNITV WASHINGTON.	
PI	Loeb LA, Black ME;	
XX	WPI; 2003-045581/04.	
DR		
XX		
PT	Novel Herpesviridae thymidine kinase mutant useful for inhibiting	
PT	pathogens e.g. viruses, bacteria, tumor in animals, has one or more	
PT	mutations encoding amino acid substitutions upstream from the DRH	
PT	nucleoside binding site.	
XX		
PS	Disclosure; Col 91-92; 78pp; English.	
XX		
CC	The invention describes an isolated Herpesviridae thymidine kinase (TK)	
CC	comprising a 12 amino acid (aa) nucleoside binding region having a site 3	
CC	made up of a DRH nucleoside binding site and a site 4 and mutation(s), at	
CC	least one of the mutations being an aa substitution 2 or 3 aa upstream or	
CC	5 or more aa downstream from the DRH motif that increases a biological	
CC	activity, preferably ability of TK to phosphorylate a nucleoside	
CC	analogue, as compared to unmutated TK. TK mutants are useful for	
CC	inhibiting a pathogenic agent such as viruses, bacteria, parasites, TK	
CC	tumour cells or autoreactive immune cells in a warm-blooded animal. TK	
CC	mutant is useful for inhibiting a tumour or cancer in a warm-blooded	
CC	animal, for treating a variety of disease e.g., hyperkeratosis	
CC	(psoriasis), prostate hypertrophy, hyperthyroidism, endocrinopathies,	
CC	autoimmune diseases, allergies, retinosis, viral diseases such as	
CC	acquired immunodeficiency syndrome (AIDS) hepatitis (HCV or HBV),	
CC	intraocular parasitic diseases, and to correct aberrant expression of a	
CC	gene within a cell, or to replace a specific gene which is defective in	
CC	proper expression using gene therapy, e.g. including adenosine deaminase	
CC	deficiency, and Alzheimer's diseases. The mutants are utilised as a	
CC	conditionally lethal marker for homologous recombination. This is the	
CC	amino acid sequence of a herpesviridae thymidine kinase (TK) mutant	
XX	peptide	
XX		
SQ	Sequence 12 AA;	
	Query Match 46.0%; Score 29; DB 6; Length 12;	
	Best Local Similarity 50.0%; Pred. No. 2.7e+02;	
	Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0	
OY	2 YGERFPDENT 11	
	: : : : :	
DB	2 WGDGRHPEKRP 11	

ID	AD C43381 standard; peptide; 8 AA.
XX	
AC	ADC43381;
XX	
DT	18-DEC-2003 (first entry)
DE	
XX	
XX	Variola smallpox virus A10L YPXL motif containing peptide, SEQ ID NO 477.
KW	viral; YPXL; cellular protein AP-50; hepatitis C virus; HCV;
KM	herpes simplex virus; HSV; UL42 protein; variola virus A10L;
KX	vaccinia virus vitron core protein Paa;
KV	human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;
KW	viral budding; viral infectivity.
XX	
OS	Variola virus.
FN	WO2003017943-A2.
XX	
PD	06-MAR-2003.
XX	
PZ	22-AUG-2002; 2002MO-US027066.
XX	
PR	22-AUG-2001; 2001US-0314182P.
XX	
PA	(MYRI-) MYRIAD GENETICS INC.
PI	Morham S, Zavitz K, Hobden A;
DR	WPI; 2003-371696/35.
XX	
PT	Novel peptide, comprising a contiguous amino acid sequence of a viral
PT	protein, capable of binding to a region of cellular protein AP-50 is
PT	useful for treating viral infections.
XX	
PS	Claim 31; SEQ ID NO 477; 60bp; English.
XX	
CC	The invention relates to a novel isolated peptide comprising a contiguous
CC	amino acid sequence of 7-30 amino acid residues of a viral protein, where
CC	the contiguous amino acid sequence encompasses the YPXL motif of the
CC	viral protein, and the 7-30 amino acid viral protein is capable of
CC	binding a region including the amino acid residues 121-435 of cellular
CC	protein AP-50. The isolated 7-30 amino acid viral protein is selected
CC	from hepatitis C virus (HCV) polypeptide, herpes simplex virus (HSV) UL42
CC	protein, variola virus A10L protein, vaccinia virus vitron core protein
CC	Paa, and human parainfluenza virus haemagglutinin-neuraminidase, where
CC	the contiguous amino acid sequence encompasses the YPXL motif of the viral
CC	protein. The peptides of the invention are useful in the manufacture of a
CC	medicament for treating viral infections caused by a virus selected from
CC	HCV, HSP-1 and variola virus. The peptides are also useful for inhibiting
CC	viral budding from virus-infected cells and/or inhibiting viral
CC	infectivity, thus inhibiting viral propagation in the cells. This
CC	sequence represents a Variola smallpox virus A10L YPXL motif containing
CC	peptide used in the treatment of viral infections of the invention.
XX	
SQ	Sequence 8 AA;
Query Match	44.4%; Score 28; DB 7; Length 8;
Best Local Similarity	50.0%; Pred. No. 1.4e+06;
Matches	4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY	4 ERFPDENF 11 :::    1 KKYPDLNF 8
Do	
RESULT 13	
AAU68482	AAU68482 standard; peptide; 9 AA.
AC	AAU68482;
XX	
DT	16-JAN-2002 (first entry)
XX	

DB Human Breast cancer-associated protein isoform, BPI-270 peptide #2.  
XX  
XX Human; Breast cancer-associated protein isoform; breast cancer;  
KW immunogen; cytostatic; BPI; tryptic digest peptide.  
XX  
XX Homo sapiens.  
OS  
XX WO200171357-A2.  
XX  
XX 27-SEP-2001.  
PD  
XX 20-MAR-2001; 2001WO-GB001219.  
PF  
XX 20-MAR-2000; 2000GB-00006695.  
PR  
XX 24-MAR-2000; 2000GB-00007265.  
XX  
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
PA  
XX Herath EMAC, O'hare NJ, Page MJ, Parekh RB, Waterfield MD;  
PI  
XX WPI; 2001-611532/70.  
DR  
XX Identifying proteins for clinical screening, diagnosis and prognosis of  
PT breast cancer, comprises detecting Breast Cancer-Associated Protein  
PT Isoforms (BPIs) using two-dimensional electrophoresis.  
FT  
XX  
XX Claim 9; Page 53; 197pp; English.  
PS  
XX The invention relates to diagnosing, determining the stage or severity,  
CC or identifying the risk of a subject developing cancer (especially breast  
CC cancer), or monitoring the effect of therapy on a subject with cancer,  
CC comprising analysing a test sample using two-dimensional electrophoresis  
CC and detecting Breast Cancer-Associated Protein Isoforms (BPIs). The  
CC methods disclosed are used for the diagnosis and prognosis of breast  
CC cancer, for determining the severity of breast cancer, and for  
CC identifying a subject at risk of developing breast cancer, and monitoring  
CC the effect of therapy administered to a subject. Antibodies raised  
CC against the binding domain of a BPI, the binding domain of a BPI, a  
CC nucleic acid encoding a BPI, or a nucleic acid that inhibits the function  
CC of a BPI can be incorporated into a pharmaceutical composition for  
CC treating or preventing breast cancer. The methods use sensitive and  
CC specific biomarkers provide early diagnosis of breast cancer, and the  
CC compositions are more potent, specific, and has a more rapid effect with  
CC fewer side effects than other prior art methods. The present sequence is  
CC a tryptic digest peptide from a BPI of the invention  
CC  
XX  
XX Sequence 9 AA;  
SQ  
Query Match 44.4%; Score 28; DB 4; Length 9;  
Best Local Similarity 83.3%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 6 PPDENF 11  
DB 1 FEDENF 6

XX  
XX WO200140312-A2.  
PN  
XX  
XX 07-JUN-2001.  
PD  
XX  
XX 04-DEC-2000; 2000WO-GB004629.  
PF  
XX  
XX 03-DEC-1999; 99GB-00028789.  
PR  
XX  
XX (DIVE-) DIVERSYS LTD.  
PA  
XX  
XX Holt LJ, De Wildt RMT, Tomlinson I;  
PI  
XX WPI; 2001-374801/39.  
DR  
XX  
XX Isolating a polypeptide of interest from a naive polypeptide repertoire  
PT which has not been preselected with a specific target ligand involves  
PT direct screening of naive polypeptide repertoire with the target ligand.  
XX  
XX Example 2; Page 29; 41pp; English.  
PS  
XX  
XX The invention relates to isolating, from a naive polypeptide (I)  
CC repertoire (antibody or T-cell receptor polypeptides), which has not been  
CC preselected with a specific target ligand, a polypeptide of interest (II)  
CC capable of interacting with the specific target ligand. The method  
CC involves direct screening of (I) with the target ligand in order to  
CC identify (II). The polypeptides selected by the method may be used in any  
CC process which involves ligand-polypeptide binding including in vivo  
CC therapeutic and prophylactic applications, in vitro and in vivo  
CC diagnostic applications, in vitro assay and reagent applications. Enzyme  
CC variants generated and selected by the method may be assayed for  
CC activity, either in vitro or in vivo using standard techniques. Antibody  
CC polypeptides selected by the method are used diagnostically in Western  
CC analysis and in situ protein detection. The selected antibodies are  
CC useful for preventing, suppressing or treating inflammatory states,  
CC allergic hypersensitivity, cancer, bacterial or viral infection and  
CC autoimmune disorders e.g., type I diabetes, multiple sclerosis,  
CC rheumatoid arthritis, systemic lupus erythematosus, Crohn's disease and  
CC myasthenia gravis. The selected polypeptides may be used extracorporeally  
CC or in vitro selectively to kill, deplete or effectively remove a target  
CC cell population from a heterogeneous collection of cells. Sequences  
CC AAB84968-979 represent complementary determining regions (CDRs) of scFv  
CC heavy and light chains binding to target antigens M and D  
CC  
XX  
XX Sequence 9 AA;  
SQ  
Query Match 44.4%; Score 28; DB 4; Length 9;  
Best Local Similarity 83.3%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 3 GERFPD 8  
DB 3 GERFPD 8

RESULT 14  
AAB84975  
ID AAB84975 standard; protein; 9 AA.  
XX  
XX AAB84975;  
AC  
XX  
XX 06-AUG-2001 (first entry)  
DT  
XX  
XX Clone 2 scFv CDR L3 region binding to target antigen D.  
DB  
XX Antinflammatory; antiallergic; cytostatic; antibacterial; antiviral;  
KW immunosuppressive; antidiabetic; neuroprotective; antirheumatic;  
KW antichratic; dermatological; immune response; modulator; enzyme;  
KW antigen D; T-cell receptor; complementary determining region; CDR.  
OS  
XX Homo sapiens.

RESULT 15  
ABG67487  
ID ABG67487 standard; peptide; 9 AA.  
XX  
XX ABG67487;  
AC  
XX  
XX 07-OCT-2002 (first entry)  
DT  
XX  
XX Human ADPI tryptic digest peptide #196.  
DB  
XX Human; Alzheimer's disease; AD; brain tissue; ADP; ADP;  
KW Alzheimer's disease-associated feature; neuroprotective;  
KW Alzheimer's disease-associated protein isoform; nootropic;  
KW ADPI tryptic digest peptide.  
OS  
XX Homo sapiens.  
XX  
XX WO200246767-A2.

XX 13-JUN-2002.  
 PD 29-NOV-2001; 2001WO-GB005289.  
 PF 08-DEC-2000; 2000US-0254431P.  
 PR (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
 PA Herath HMAc, Parekh RB, Rohlf C;  
 PI WPI, 2002-508575/54.  
 DR Screening, diagnosis or prognosis of Alzheimer's disease in subject,  
 PT comprises detecting Alzheimer disease-associated features or Alzheimer  
 PT disease-associated protein isoforms in brain tissue from the subject.  
 PS Claim 7; Page 72; 427pp; English.  
 XX The present invention relates to methods and compositions for the  
 CC screening, diagnosis or prognosis of Alzheimer's disease (AD) in a  
 CC subject. The method comprises analysing a sample of brain tissue from a  
 CC subject by 2D electrophoresis to generate a 2D array of Alzheimer's  
 CC disease-associated features (ADFs), whose relative abundance correlates  
 CC with the presence, absence, stage or severity of AD and comparing the  
 CC abundance of each feature with the abundance of that chosen feature in  
 CC brain tissue from persons free from AD. The invention also describes  
 CC Alzheimer's disease-associated protein isoforms (ADPIs) detectable in  
 CC brain tissue. The methods and compositions of the invention are useful  
 CC for the screening, diagnosis or prognosis of AD in a subject, for  
 CC determining the stage or severity of AD in a subject, for identifying a  
 CC subject at risk of developing AD, or for monitoring the effect of therapy  
 CC administered to a subject having AD. Antibodies capable of binding to  
 CC ADPIs are useful for treating or preventing AD, and for determining the  
 CC efficacy of a given treatment regime. An agent that modulates the  
 CC activity of ADPI is useful in the manufacture of a medicament for the  
 CC treatment or prevention of AD in a subject. AEG67292-ABG68038 represent  
 CC human ADPI tryptic digest peptides  
 CC  
 CC Sequence 9 AA;  
 SQ  
 Query Match 44.4%; Score 28; DB 5; Length 9;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 6 FEDENF 11  
 DB 1 FEDENF 6  
 RESULT 16  
 ABR58800  
 ID ABR58800 standard; peptide; 9 AA.  
 AC ABR58800;  
 XX 11-JUN-2003 (first entry)  
 DT  
 XX Alzheimer's Disease-associated protein isoform, APT-333, SEQ ID 118.  
 DE  
 XX Noctropic; Neuroprotective; Alzheimer's disease; AD; human;  
 KW Alzheimer's Disease-associated protein isoform.  
 XX Homo sapiens.  
 OS  
 XX WO2003028543-A2.  
 FN  
 XX 10-APR-2003.  
 PD  
 XX 03-OCT-2002; 2002WO-US031642.  
 PF  
 XX 03-OCT-2001; 2001US-0326708P.  
 PR  
 XX

PA (PRIZ ) PRIZER PROD INC.  
 PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
 XX Durham UK, Friedman DL, Herath HMAc, Kimmel LH, Parekh RB;  
 PI Potter DM, Rohlf C, Silber BM, Snyder PJ, Soares HD, Stiger TR;  
 PI Sunderland PT, Townsend RR, White WF, Williams SA;  
 XX WPI, 2003-371957/35.  
 DR Screening or diagnosing of Alzheimer's disease (AD) determine the stage  
 PT or severity of AD in a subject, comprises analyzing a test sample of body  
 PT fluid from the subject by 2-dimensional electrophoresis.  
 XX  
 PS Claim 2; Page 34; 179pp; English.  
 CC The present invention relates to methods for screening or diagnosing  
 CC Alzheimer's disease (AD) to determine the stage or severity of AD in a  
 CC subject, to identify subject at risk of developing AD, or to monitor the  
 CC effect of therapy administered. The methods comprise analysing a test  
 CC sample of body fluid by 2-dimensional electrophoresis to generate a 2-  
 CC dimensional array of AD-associated features (AFs). The method  
 CC alternatively comprises quantitatively detecting in a sample of body  
 CC fluid from the subject, one or more AD-associated protein isoforms (ADPIs;  
 CC ABR58710-ABR59184)  
 CC  
 CC Sequence 9 AA;  
 SQ  
 Query Match 44.4%; Score 28; DB 6; Length 9;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 6 FEDENF 11  
 DB 1 FEDENF 6  
 RESULT 17  
 ADA23600  
 ID ADA23600 standard; peptide; 9 AA.  
 AC ADA23600;  
 XX 20-NOV-2003 (first entry)  
 DT  
 XX Alzheimer's disease-associated protein isoform tryptic peptide #209.  
 DE  
 XX human; Alzheimer's disease; vascular dementia; Lewy body dementia;  
 KW schizophrenia; Parkinson's disease; multiple sclerosis; depression;  
 KW Alzheimer's disease-associated protein isoform, ADPI.  
 XX  
 OS Homo sapiens.  
 XX US2003064411-A1.  
 PN  
 XX 03-APR-2003.  
 PD  
 XX 10-DEC-2001; 2001US-00014340.  
 PF  
 XX 08-DEC-2000; 2000US-0254431P.  
 PR  
 XX (HERA/) HERATH H M A C.  
 PA (PARE/) PAREKH R B.  
 PA (ROHL/) ROHLF C.  
 XX Herath HMAc, Parekh RB, Rohlf C;  
 PI WPI, 2003-540784/51.  
 DR  
 XX Screening, diagnosis or prognosis of Alzheimer's disease in subject,  
 PT involves analyzing test sample of brain tissue from subject, and  
 PT comparing feature in test sample with that of person(s) free from  
 PT Alzheimer's disease.  
 XX

PS Disclosure; SEQ ID NO 209; 115bp; English.

XX

CC The invention relates to a method of screening or diagnosing Alzheimer's disease in a subject. The method is useful for screening, diagnosis or prognosis of Alzheimer's disease in a subject for determining the stage of severity of Alzheimer's disease in a subject, for identifying a subject at risk of developing Alzheimer's disease, or for monitoring the effect of therapy administered to a subject having Alzheimer's disease. The method is also useful in treating vascular dementia, Lewy body dementia, schizophrenia, Parkinson's disease, multiple sclerosis or depression. The inventive method identifies sensitive and specific biomarkers for the diagnosis of Alzheimer's disease in living subjects. It provides therapeutic agents for Alzheimer's disease that work quickly, potentially, specifically with fewer side effects. The present sequence represents the amino acid sequence of a Alzheimer's disease-associated protein isoform tryptic peptide.

CC

XX

Sequence 9 AA:

SO

Query Match 44.4%; Score 28; DB 6; Length 9;  
Best Local Similarity 83.3%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 FPDENP 11  
| | | | |  
1 FEDENF 6

Db

RESULT 18

ABR62869

ID ABR62869 standard; peptide; 9 AA.

XX

AC ABR62869;

DT 04-DEC-2003 (first entry)

XX

DB Tumourigenesis, metastasis-associated T cell cyclophilin peptide.

XX

KM Cyclophilin; peptidyl-prolyl cis-trans isomerase; enzyme; tumourigenesis; metastasis; cancer; diagnosis; human.

XX

OS Homo sapiens.

XX

PN WO2003060522-A1.

XX

PD 24-JUL-2003.

XX

PF 28-DEC-2002; 2002WO-KR002469.

XX

PR 29-DEC-2001; 2001KR-0008090.

XX

PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.

XX

PI Ko JH, Hwang SY, Sohn H, Oh S, Lee JH, Lee SC, Yoo J, Lee D;

XX

DR WPI; 2003-646050/61.

XX

PT Diagnosing cancers by measuring the changes of N-linked sugar chains of proteins related to tumorigenesis and metastasis, including cancers of the large intestine, stomach, lung, liver, uterus, breast and pancreas.

XX

PS Example 3; Page 42; 49pp; English.

XX

CC The present sequence is a peptide fragment of T cell cyclophilin (peptidyl-prolyl cis-trans isomerase). Changes in glycosylation of this protein are associated with metastasis and tumorigenesis. The protein has 3 preserved N-linked sugar chain sites. A method for diagnosing cancer involves measuring changes of sugar chains of proteins related to tumorigenesis and metastasis. The changes are especially changes of sugar chain branches of N-linked beta-1,6 N-acetylglucosamine. The protein is prostate-derived factor, peptidyl-prolyl cis-trans isomerase, galectin binding protein, I3 antigen, Mac-2-binding protein, serum protein 90K, tumour associated antigen 90K, TIMP-1 and a novel, unidentified protein.

CC

CC The cancer is large intestine cancer, stomach cancer, lung cancer, liver cancer, uterine cancer, breast cancer and pancreas cancer

CC

XX

Sequence 9 AA:

SO

Query Match 44.4%; Score 28; DB 7; Length 9;  
Best Local Similarity 83.3%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 FPDENP 11  
| | | | |  
1 FEDENP 6

Db

RESULT 19

ADC43382

ID ADC43382 standard; peptide; 9 AA.

XX

AC ADC43382;

DT 18-DEC-2003 (first entry)

XX

DE Variola smallpox virus A10L YPXL motif containing peptide, SEQ ID No 476.

XX

KM viral; YPXL; cellular protein AP-50; hepatitis C virus; HCV; herpes simplex virus; HSV; UL42 protein; variola virus A10L; KW vaccinia virus virion core protein P4a; KM human parainfluenza virus haemagglutinin-neuraminidase; HSP-1; KM viral budding; viral infectivity.

XX

OS Variola virus.

XX

PN WO2003017943-A2.

XX

PD 06-MAR-2003.

XX

PF 22-AUG-2002; 2002WO-US027066.

XX

PR 22-AUG-2001; 2001US-0314182P.

XX

PA (MYRI-) MYRIAD GENETICS INC.

XX

PI Morham S, Zavitz K, Hobden A;

XX

DR WPI; 2003-371636/35.

XX

PT Novel peptide, comprising a contiguous amino acid sequence of a viral protein, capable of binding to a region of cellular protein AP-50 is useful for treating viral infections.

XX

PS Claim 31; SEQ ID NO 478; 60pp; English.

XX

CC The invention relates to a novel isolated peptide comprising a contiguous amino acid sequence of 7-30 amino acid residues of a viral protein, where the contiguous amino acid sequence encompasses the YPXL motif of the viral protein, and the 7-30 amino acid viral protein is capable of binding a region including the amino acid residues 121-435 of cellular protein AP-50. The isolated 7-30 amino acid viral protein is selected from hepatitis C virus (HCV) polypeptide, herpes simplex virus (HSV) UL42 protein, variola virus A10L protein, vaccinia virus virion core protein P4a, and human parainfluenza virus haemagglutinin-neuraminidase, where the contiguous amino acid sequence encompasses the YPXL motif of the viral protein. The peptides of the invention are useful in the manufacture of a medicament for treating viral infections caused by a virus selected from HCV, HSP-1 and variola virus. The peptides are also useful for inhibiting viral budding from virus-infected cells and/or inhibiting viral infectivity, thus inhibiting viral propagation in the cells. This sequence represents a Variola smallpox virus A10L YPXL motif containing peptide used in the treatment of viral infections of the invention.

CC

XX

Sequence 9 AA;

SO

Query Match 44.4%; Score 28; DB 7; Length 9;

Best Local Similarity 50.0%; Pred. No. 1.4e+06;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPDENF 11  
DB 1 KKYPDLPNF 8

## RESULT 20

ID ADC43395 standard; peptide; 9 AA.

XX AD43395;

DT 18-DEC-2003 (first entry)

DE Variola smallpox virus A10L YPXL motif containing peptide, SEQ ID NO 491.

XX viral; YPXL; cellular protein AP-50; hepatitis C virus; HCV;  
KM herpes simplex virus; HSV; UL42 protein; variola virus A10L;  
KM vaccinia virus viron core protein P4a;  
KM human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;  
KM viral budding; viral infectivity.

OS Variola virus.

PN WO2003017943-A2.

PD 06-MAR-2003.

PF 22-AUG-2002; 2002WO-US027066.

PR 22-AUG-2001; 2001US-0314182P.

PA (MYRI-) MYRIAD GENETICS INC.

PI Morham S, Zavitz K, Hobden A;

DR WPI; 2003-371696/35.

XX Novel peptide, comprising a contiguous amino acid sequence of a viral  
PT protein, capable of binding to a region of cellular protein AP-50 is  
PT useful for treating viral infections.

PS Claim 31; SEQ ID NO 491; 60pp; English.

XX The invention relates to a novel isolated peptide comprising a contiguous  
CC amino acid sequence of 7-30 amino acid residues of a viral protein, where  
CC the contiguous amino acid sequence encompasses the YPXL motif of the  
CC viral protein, and the 7-30 amino acid viral protein is capable of  
CC binding a region including the amino acid residues 121-435 of cellular  
CC protein AP-50. The isolated 7-30 amino acid viral protein is selected  
CC from hepatitis C virus (HCV) polypeptide, herpes simplex virus (HSV) UL42  
CC protein, variola virus A10L protein, vaccinia virus viron core protein  
CC P4a, and human parainfluenza virus haemagglutinin-neuraminidase, where  
CC the contiguous amino acid sequence encompasses the YPXL motif of the viral  
CC protein. The peptides of the invention are useful in the manufacture of a  
CC medicament for treating viral infections caused by a virus selected from  
CC HCV, HSP-1 and variola virus. The peptides are also useful for inhibiting  
CC viral budding from virus-infected cells and/or inhibiting viral  
CC infectivity, thus inhibiting viral propagation in the cells. This  
CC sequence represents a Variola smallpox virus A10L YPXL motif containing  
CC peptide used in the treatment of viral infections of the invention.

XX Sequence 9 AA;

Query Match 44.4%; Score 28; DB 7; Length 9;  
Best Local Similarity 50.0%; Pred. No. 1.4e+06;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPDENF 11  
DB 2 KKYPDLPNF 9

## RESULT 21

ID ADC43396 standard; peptide; 10 AA.

XX AD43396;

DT 18-DEC-2003 (first entry)

DE Variola smallpox virus A10L YPXL motif containing peptide, SEQ ID NO 492.

XX viral; YPXL; cellular protein AP-50; hepatitis C virus; HCV;  
KM herpes simplex virus; HSV; UL42 protein; variola virus A10L;  
KM vaccinia virus viron core protein P4a;  
KM human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;  
KM viral budding; viral infectivity.

OS Variola virus.

PN WO2003017943-A2.

PD 06-MAR-2003.

PF 22-AUG-2002; 2002WO-US027066.

PR 22-AUG-2001; 2001US-0314182P.

PA (MYRI-) MYRIAD GENETICS INC.

PI Morham S, Zavitz K, Hobden A;

DR WPI; 2003-371696/35.

XX Novel peptide, comprising a contiguous amino acid sequence of a viral  
PT protein, capable of binding to a region of cellular protein AP-50 is  
PT useful for treating viral infections.

PS Claim 31; SEQ ID NO 492; 60pp; English.

XX The invention relates to a novel isolated peptide comprising a contiguous  
CC amino acid sequence of 7-30 amino acid residues of a viral protein, where  
CC the contiguous amino acid sequence encompasses the YPXL motif of the  
CC viral protein, and the 7-30 amino acid viral protein is capable of  
CC binding a region including the amino acid residues 121-435 of cellular  
CC protein AP-50. The isolated 7-30 amino acid viral protein is selected  
CC from hepatitis C virus (HCV) polypeptide, herpes simplex virus (HSV) UL42  
CC protein, variola virus A10L protein, vaccinia virus viron core protein  
CC P4a, and human parainfluenza virus haemagglutinin-neuraminidase, where  
CC the contiguous amino acid sequence encompasses the YPXL motif of the viral  
CC protein. The peptides of the invention are useful in the manufacture of a  
CC medicament for treating viral infections caused by a virus selected from  
CC HCV, HSP-1 and variola virus. The peptides are also useful for inhibiting  
CC viral budding from virus-infected cells and/or inhibiting viral  
CC infectivity, thus inhibiting viral propagation in the cells. This  
CC sequence represents a Variola smallpox virus A10L YPXL motif containing  
CC peptide used in the treatment of viral infections of the invention.

XX Sequence 10 AA;

Query Match 44.4%; Score 28; DB 7; Length 10;  
Best Local Similarity 50.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPDENF 11  
DB 2 KKYPDLPNF 9

## RESULT 22

ID ADC43409 standard; peptide; 10 AA.

XX

AC ADC43409;  
XX 18-DEC-2003 (first entry)  
XX  
DE Variola smallpox virus A10L YPXL motif containing peptide, SEQ ID NO 505.  
XX  
KM viral; YPXL; cellular protein AP-50; hepatitis C virus; HCV;  
KM herpes simplex virus; HSV; UL42 protein; variola virus A10L;  
KM vaccinia virus virion core protein P4a;  
KM human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;  
KM viral budding; viral infectivity.  
XX  
OS Variola virus.  
XX WO2003017943-A2.  
XX  
PD 06-MAR-2003.  
XX  
XX 22-AUG-2002; 2002WO-US027066.  
XX  
XX 22-AUG-2001; 2001US-0314182P.  
XX  
PA (MTRI-) MTRIAD GENETICS INC.  
XX  
PI Morham S, Zavitz K, Hobden A;  
XX  
DR WPI; 2003-371696/35.  
XX  
PT Novel peptide, comprising a contiguous amino acid sequence of a viral  
PT protein, capable of binding to a region of cellular protein AP-50 is  
PT useful for treating viral infections.  
XX  
PS Claim 31; SEQ ID NO 505; 60pp; English.  
XX  
CC The invention relates to a novel isolated peptide comprising a contiguous  
CC amino acid sequence of 7-30 amino acid residues of a viral protein, where  
CC the contiguous amino acid sequence encompasses the YPXL motif of the  
CC viral protein, and the 7-30 amino acid viral protein is capable of  
CC binding a region including the amino acid residues 121-435 of cellular  
CC protein AP-50. The isolated 7-30 amino acid viral protein is selected  
CC from hepatitis C virus (HCV) polypeptide, herpes simplex virus (HSV) UL42  
CC protein, variola virus A10L protein, vaccinia virus virion core protein  
CC P4a, and human parainfluenza virus haemagglutinin-neuraminidase, where  
CC the contiguous amino acid sequence encompasses the YPXL motif of the viral  
CC protein. The peptides of the invention are useful in the manufacture of a  
CC medicament for treating viral infections caused by a virus selected from  
CC HCV, HSP-1 and variola virus. The peptides are also useful for inhibiting  
CC viral budding from virus-infected cells and/or inhibiting viral  
CC infectivity, thus inhibiting viral propagation in the cells. This  
CC sequence represents a Variola smallpox virus A10L YPXL motif containing  
CC peptide used in the treatment of viral infections of the invention.  
XX  
SQ Sequence 10 AA;  
Query Match 44.4%; Score 28; DB 7; Length 10;  
Best Local Similarity 50.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPDENF 11  
: : : : :  
Db 3 KKYPDLENF 10

RESULT 23  
ADC43383  
XX ADC43383 standard; peptide; 10 AA.  
XX  
AC ADC43383;  
XX  
XX 18-DEC-2003 (first entry)  
XX  
XX Variola smallpox virus A10L YPXL motif containing peptide, SEQ ID NO 479.  
XX

KM viral; YPXL; cellular protein AP-50; hepatitis C virus; HCV;  
KM herpes simplex virus; HSV; UL42 protein; variola virus A10L;  
KM vaccinia virus virion core protein P4a;  
KM human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;  
KM viral budding; viral infectivity.  
XX  
OS Variola virus.  
XX WO2003017943-A2.  
XX  
PD 06-MAR-2003.  
XX  
XX 22-AUG-2002; 2002WO-US027066.  
XX  
XX 22-AUG-2001; 2001US-0314182P.  
XX  
PA (MTRI-) MTRIAD GENETICS INC.  
XX  
PI Morham S, Zavitz K, Hobden A;  
XX  
DR WPI; 2003-371696/35.  
XX  
PT Novel peptide, comprising a contiguous amino acid sequence of a viral  
PT protein, capable of binding to a region of cellular protein AP-50 is  
PT useful for treating viral infections.  
XX  
PS Claim 31; SEQ ID NO 479; 60pp; English.  
XX  
CC The invention relates to a novel isolated peptide comprising a contiguous  
CC amino acid sequence of 7-30 amino acid residues of a viral protein, where  
CC the contiguous amino acid sequence encompasses the YPXL motif of the  
CC viral protein, and the 7-30 amino acid viral protein is capable of  
CC binding a region including the amino acid residues 121-435 of cellular  
CC protein AP-50. The isolated 7-30 amino acid viral protein is selected  
CC from hepatitis C virus (HCV) polypeptide, herpes simplex virus (HSV) UL42  
CC protein, variola virus A10L protein, vaccinia virus virion core protein  
CC P4a, and human parainfluenza virus haemagglutinin-neuraminidase, where  
CC the contiguous amino acid sequence encompasses the YPXL motif of the viral  
CC protein. The peptides of the invention are useful in the manufacture of a  
CC medicament for treating viral infections caused by a virus selected from  
CC HCV, HSP-1 and variola virus. The peptides are also useful for inhibiting  
CC viral budding from virus-infected cells and/or inhibiting viral  
CC infectivity, thus inhibiting viral propagation in the cells. This  
CC sequence represents a Variola smallpox virus A10L YPXL motif containing  
CC peptide used in the treatment of viral infections of the invention.  
XX  
SQ Sequence 10 AA;  
Query Match 44.4%; Score 28; DB 7; Length 10;  
Best Local Similarity 50.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPDENF 11  
: : : : :  
Db 1 KKYPDLENF 8

RESULT 24  
ADC43397  
XX ADC43397 standard; peptide; 11 AA.  
XX  
AC ADC43397;  
XX  
XX 18-DEC-2003 (first entry)  
XX  
XX Variola smallpox virus A10L YPXL motif containing peptide, SEQ ID NO 493.  
XX  
DE viral; YPXL; cellular protein AP-50; hepatitis C virus; HCV;  
XX  
XX herpes simplex virus; HSV; UL42 protein; variola virus A10L;  
XX  
XX vaccinia virus virion core protein P4a;  
XX  
XX human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;  
XX  
XX viral budding; viral infectivity.





PI Morham S, Zavitz K, Hobden A;  
XX  
DR WPI; 2003-371696/35.  
XX  
PT Novel peptide, comprising a contiguous amino acid sequence of a viral  
PT protein, capable of binding to a region of cellular protein AP-50 is  
PT useful for treating viral infections.  
XX  
PS Claim 31; SEQ ID NO 480; 60pp; English.  
XX  
CC The invention relates to a novel isolated peptide comprising a contiguous  
CC amino acid sequence of 7-30 amino acid residues of a viral protein, where  
CC the contiguous amino acid sequence encompasses the YPKL motif of the  
CC viral protein, and the 7-30 amino acid viral protein is capable of  
CC binding a region including the amino acid residues 121-435 of cellular  
CC protein AP-50. The isolated 7-30 amino acid viral protein is selected  
CC from hepatitis C virus (HCV) polypeptide, herpes simplex virus (HSV) UL42  
CC protein, variola virus A10L protein, vaccinia virus virion core protein  
CC P4a, and human parainfluenza virus haemagglutinin-neuraminidase, where  
CC the contiguous amino acid sequence encompasses the YPKL motif of the viral  
CC protein. The peptides of the invention are useful in the manufacture of a  
CC medicament for treating viral infections caused by a virus selected from  
CC HCV, HSP-1 and variola virus. The peptides are also useful for inhibiting  
CC viral budding from virus-infected cells and/or inhibiting viral  
CC infectivity, thus inhibiting viral propagation in the cells. This  
CC sequence represents a Variola smallpox virus A10L YPKL motif containing  
CC peptide used in the treatment of viral infections of the invention.  
XX  
SQ Sequence 11 AA;  
XX  
Query Match 44.4%; Score 28; DB 7; Length 11;  
Best Local Similarity 50.0%; Pred. No. 3.7e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
XX  
QY 4 ERPPDENF 11  
Db 1 KKYVDLNF 8  
XX  
RESULT 27  
ADC43422  
ID ADC43422 standard; peptide; 11 AA.  
XX  
AC ADC43422;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE Variola smallpox virus A10L YPKL motif containing peptide, SEQ ID No 518.  
XX  
KM viral; YPKL; cellular protein AP-50; hepatitis C virus; HCV;  
KM herpes simplex virus; HSV; UL42 protein; variola virus A10L;  
KM vaccinia virus virion core protein P4a;  
KM human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;  
KM viral budding; viral infectivity.  
XX  
OS Variola virus.  
XX  
PN WO2003017943-A2.  
XX  
PD 06-MAR-2003.  
XX  
PF 22-AUG-2002; 2002MO-US027066.  
XX  
PR 22-AUG-2001; 2001US-0314182P.  
XX  
PA (MYRI-) MYRIAD GENETICS INC.  
XX  
PI Morham S, Zavitz K, Hobden A;  
XX  
DR WPI; 2003-371696/35.  
XX  
PT Novel peptide, comprising a contiguous amino acid sequence of a viral  
PT protein, capable of binding to a region of cellular protein AP-50 is

PT useful for treating viral infections.  
XX  
PS Claim 31; SEQ ID NO 518; 60pp; English.  
XX  
CC The invention relates to a novel isolated peptide comprising a contiguous  
CC amino acid sequence of 7-30 amino acid residues of a viral protein, where  
CC the contiguous amino acid sequence encompasses the YPKL motif of the  
CC viral protein, and the 7-30 amino acid viral protein is capable of  
CC binding a region including the amino acid residues 121-435 of cellular  
CC protein AP-50. The isolated 7-30 amino acid viral protein is selected  
CC from hepatitis C virus (HCV) polypeptide, herpes simplex virus (HSV) UL42  
CC protein, variola virus A10L protein, vaccinia virus virion core protein  
CC P4a, and human parainfluenza virus haemagglutinin-neuraminidase, where  
CC the contiguous amino acid sequence encompasses the YPKL motif of the viral  
CC protein. The peptides of the invention are useful in the manufacture of a  
CC medicament for treating viral infections caused by a virus selected from  
CC HCV, HSP-1 and variola virus. The peptides are also useful for inhibiting  
CC viral budding from virus-infected cells and/or inhibiting viral  
CC infectivity, thus inhibiting viral propagation in the cells. This  
CC sequence represents a Variola smallpox virus A10L YPKL motif containing  
CC peptide used in the treatment of viral infections of the invention.  
XX  
SQ Sequence 11 AA;  
XX  
Query Match 44.4%; Score 28; DB 7; Length 11;  
Best Local Similarity 50.0%; Pred. No. 3.7e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
XX  
QY 4 ERPPDENF 11  
Db 4 KKYVDLNF 11  
XX  
RESULT 28  
ADC43411  
ID ADC43411 standard; peptide; 12 AA.  
XX  
AC ADC43411;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE Variola smallpox virus A10L YPKL motif containing peptide, SEQ ID No 507.  
XX  
KM viral; YPKL; cellular protein AP-50; hepatitis C virus; HCV;  
KM herpes simplex virus; HSV; UL42 protein; variola virus A10L;  
KM vaccinia virus virion core protein P4a;  
KM human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;  
KM viral budding; viral infectivity.  
XX  
OS Variola virus.  
XX  
PN WO2003017943-A2.  
XX  
PD 06-MAR-2003.  
XX  
PF 22-AUG-2002; 2002MO-US027066.  
XX  
PR 22-AUG-2001; 2001US-0314182P.  
XX  
PA (MYRI-) MYRIAD GENETICS INC.  
XX  
PI Morham S, Zavitz K, Hobden A;  
XX  
DR WPI; 2003-371696/35.  
XX  
PT Novel peptide, comprising a contiguous amino acid sequence of a viral  
PT protein, capable of binding to a region of cellular protein AP-50 is  
PT useful for treating viral infections.  
XX  
PS Claim 31; SEQ ID NO 507; 60pp; English.  
XX  
CC The invention relates to a novel isolated peptide comprising a contiguous  
CC amino acid sequence of 7-30 amino acid residues of a viral protein, where

CC the contiguous amino acid sequence encompasses the YPXL motif of the  
 CC viral protein, and the 7-30 amino acid viral protein is capable of  
 CC binding a region including the amino acid residues 121-435 of cellular  
 CC protein AP-50. The isolated 7-30 amino acid viral protein is selected  
 CC from hepatitis C virus (HCV) polypeptide, herpes simplex virus (HSV) UL42  
 CC protein, variola virus A10L protein, vaccinia virus viron core protein  
 CC P4a, and human parainfluenza virus haemagglutinin-neuraminidase, where  
 CC the contiguous amino acid sequence encompasses the YPXL motif of the viral  
 CC protein. The peptides of the invention are useful in the manufacture of a  
 CC medicament for treating viral infections caused by a virus selected from  
 CC HCV, HSP-1 and variola virus. The peptides are also useful for inhibiting  
 CC viral budding from virus-infected cells and/or inhibiting viral  
 CC infectivity, thus inhibiting viral propagation in the cells. This  
 CC sequence represents a Variola smallpox virus A10L YPXL motif containing  
 CC peptide used in the treatment of viral infections of the invention.

CC Sequence 12 AA:

Query Match 44.4%; Score 28; DB 7; Length 12;  
 Best Local Similarity 50.0%; Pred. No. 4e+02;  
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFDPENF 11  
 : : : : :  
 Db 3 KKYDPDINF 10

RESULT 29  
 ADC43385  
 ID ADC43385 standard; peptide; 12 AA.

AC ADC43385;  
 DT 18-DEC-2003 (first entry)

DE Variola smallpox virus A10L YPXL motif containing peptide, SEQ ID No 481.

KM viral; YPXL; cellular protein AP-50; hepatitis C virus; HCV;  
 KM herpes simplex virus; HSV; UL42 protein; variola virus A10L;  
 KM vaccinia virus viron core protein P4a;  
 KM human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;  
 KM viral budding; viral infectivity.

OS Variola virus.

PM WO2003017943-A2.

PD 06-MAR-2003.

PF 22-AUG-2002; 2002WO-US027066.

PR 22-AUG-2001; 2001US-0314182P.

PA (MYRI-) MYRIAD GENETICS INC.

PI Morham S, Zavitz K, Hobden A;

PI WPI; 2003-371696/35.

DR Novel peptide, comprising a contiguous amino acid sequence of a viral  
 PT protein, capable of binding to a region of cellular protein AP-50 is  
 PT useful for treating viral infections.

PS Claim 31; SEQ ID NO 481; 60pp; English.

CC The invention relates to a novel isolated peptide comprising a contiguous  
 CC amino acid sequence of 7-30 amino acid residues of a viral protein, where  
 CC the contiguous amino acid sequence encompasses the YPXL motif of the  
 CC viral protein, and the 7-30 amino acid viral protein is capable of  
 CC binding a region including the amino acid residues 121-435 of cellular  
 CC protein AP-50. The isolated 7-30 amino acid viral protein is selected  
 CC from hepatitis C virus (HCV) polypeptide, herpes simplex virus (HSV) UL42  
 CC protein, variola virus A10L protein, vaccinia virus viron core protein

CC P4a, and human parainfluenza virus haemagglutinin-neuraminidase, where  
 CC the contiguous amino acid sequence encompasses the YPXL motif of the viral  
 CC protein. The peptides of the invention are useful in the manufacture of a  
 CC medicament for treating viral infections caused by a virus selected from  
 CC HCV, HSP-1 and variola virus. The peptides are also useful for inhibiting  
 CC viral budding from virus-infected cells and/or inhibiting viral  
 CC infectivity, thus inhibiting viral propagation in the cells. This  
 CC sequence represents a Variola smallpox virus A10L YPXL motif containing  
 CC peptide used in the treatment of viral infections of the invention.

CC Sequence 12 AA:

Query Match 44.4%; Score 28; DB 7; Length 12;  
 Best Local Similarity 50.0%; Pred. No. 4e+02;  
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFDPENF 11  
 : : : : :  
 Db 1 KKYDPDINF 8

RESULT 30  
 ADC43423  
 ID ADC43423 standard; peptide; 12 AA.

AC ADC43423;

DT 18-DEC-2003 (first entry)

DE Variola smallpox virus A10L YPXL motif containing peptide, SEQ ID No 519.

KM viral; YPXL; cellular protein AP-50; hepatitis C virus; HCV;  
 KM herpes simplex virus; HSV; UL42 protein; variola virus A10L;  
 KM vaccinia virus viron core protein P4a;  
 KM human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;  
 KM viral budding; viral infectivity.

OS Variola virus.

PM WO2003017943-A2.

PD 06-MAR-2003.

PF 22-AUG-2002; 2002WO-US027066.

PR 22-AUG-2001; 2001US-0314182P.

PA (MYRI-) MYRIAD GENETICS INC.

PI Morham S, Zavitz K, Hobden A;

PI WPI; 2003-371696/35.

DR Novel peptide, comprising a contiguous amino acid sequence of a viral  
 PT protein, capable of binding to a region of cellular protein AP-50 is  
 PT useful for treating viral infections.

PS Claim 31; SEQ ID NO 519; 60pp; English.

CC The invention relates to a novel isolated peptide comprising a contiguous  
 CC amino acid sequence of 7-30 amino acid residues of a viral protein, where  
 CC the contiguous amino acid sequence encompasses the YPXL motif of the  
 CC viral protein, and the 7-30 amino acid viral protein is capable of  
 CC binding a region including the amino acid residues 121-435 of cellular  
 CC protein AP-50. The isolated 7-30 amino acid viral protein is selected  
 CC from hepatitis C virus (HCV) polypeptide, herpes simplex virus (HSV) UL42  
 CC protein, variola virus A10L protein, vaccinia virus viron core protein  
 CC P4a, and human parainfluenza virus haemagglutinin-neuraminidase, where  
 CC the contiguous amino acid sequence encompasses the YPXL motif of the viral  
 CC protein. The peptides of the invention are useful in the manufacture of a  
 CC medicament for treating viral infections caused by a virus selected from  
 CC HCV, HSP-1 and variola virus. The peptides are also useful for inhibiting  
 CC viral budding from virus-infected cells and/or inhibiting viral

CC infectivity, thus inhibiting viral propagation in the cells. This  
CC sequence represents a Variola smallpox virus A10L YPXL motif containing  
CC peptide used in the treatment of viral infections of the invention.

XX Sequence 12 AA;

Query Match 44.4%; Score 28; DB 7; Length 12;  
Best Local Similarity 50.0%; Pred. No. 4e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERPDPENF 11  
:::| | | |  
DB 4 KKYPDLNF 11

## RESULT 31

ID ADC43434 standard; peptide, 12 AA.

AC ADC43434;

DT 18-DEC-2003 (first entry)

DE Variola smallpox virus A10L YPXL motif containing peptide, SEQ ID No 530.

XX viral; YPXL; cellular protein AP-50; hepatitis C virus; HCV;  
KW herpes simplex virus; HSV; UL42 protein; variola virus A10L;  
KW vaccinia virus virion core protein P4a;  
KW human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;  
KM viral budding; viral infectivity.

XX Variola virus.

OS WO2003017943-A2.

PN 06-MAR-2003.

PD 22-AUG-2002; 2002WO-US027066.

PF 22-AUG-2001; 2001US-0314182P.

PR (MYRI-) MYRIAD GENETICS INC.

PA Morham S, Zavitz K, Hobden A;

PI WPI; 2003-371696/35.

PS Novel peptide, comprising a contiguous amino acid sequence of a viral  
XX protein, capable of binding to a region of cellular protein AP-50 is  
XX useful for treating viral infections.

XX Claim 31; SEQ ID NO 530; 60pp; English.

XX The invention relates to a novel isolated peptide comprising a contiguous  
XX amino acid sequence of 7-30 amino acid residues of a viral protein, where  
XX the contiguous amino acid sequence encompasses the YPXL motif of the  
XX viral protein, and the 7-30 amino acid viral protein is capable of  
XX binding a region including the amino acid residues 121-435 of cellular  
XX protein AP-50. The isolated 7-30 amino acid viral protein is selected  
XX from hepatitis C virus (HCV) polypeptide, herpes simplex virus (HSV) UL42  
XX protein, variola virus A10L protein, vaccinia virus virion core protein  
XX P4a, and human parainfluenza virus haemagglutinin-neuraminidase, where  
XX the contiguous amino acid sequence encompasses the YPXL motif of the viral  
XX protein. The peptides of the invention are useful in the manufacture of a  
XX medicament for treating viral infections caused by a virus selected from  
XX HCV, HSP-1 and variola virus. The peptides are also useful for inhibiting  
XX viral budding from virus-infected cells and/or inhibiting viral  
XX infectivity, thus inhibiting viral propagation in the cells. This  
XX sequence represents a Variola smallpox virus A10L YPXL motif containing  
XX peptide used in the treatment of viral infections of the invention.

XX Sequence 12 AA;

Query Match 44.4%; Score 28; DB 7; Length 12;  
Best Local Similarity 50.0%; Pred. No. 4e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERPDPENF 11  
:::| | | |  
DB 5 KKYPDLNF 12

## RESULT 32

ID ADC43398 standard; peptide, 12 AA.

AC ADC43398;

DT 18-DEC-2003 (first entry)

DE Variola smallpox virus A10L YPXL motif containing peptide, SEQ ID No 494.

XX viral; YPXL; cellular protein AP-50; hepatitis C virus; HCV;  
KW herpes simplex virus; HSV; UL42 protein; variola virus A10L;  
KW vaccinia virus virion core protein P4a;  
KW human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;  
KM viral budding; viral infectivity.

XX Variola virus.

OS WO2003017943-A2.

PN 06-MAR-2003.

PD 22-AUG-2002; 2002WO-US027066.

PF 22-AUG-2001; 2001US-0314182P.

PR (MYRI-) MYRIAD GENETICS INC.

PA Morham S, Zavitz K, Hobden A;

PI WPI; 2003-371696/35.

PS Novel peptide, comprising a contiguous amino acid sequence of a viral  
XX protein, capable of binding to a region of cellular protein AP-50 is  
XX useful for treating viral infections.

XX Claim 31; SEQ ID No 494; 60pp; English.

XX The invention relates to a novel isolated peptide comprising a contiguous  
XX amino acid sequence of 7-30 amino acid residues of a viral protein, where  
XX the contiguous amino acid sequence encompasses the YPXL motif of the  
XX viral protein, and the 7-30 amino acid viral protein is capable of  
XX binding a region including the amino acid residues 121-435 of cellular  
XX protein AP-50. The isolated 7-30 amino acid viral protein is selected  
XX from hepatitis C virus (HCV) polypeptide, herpes simplex virus (HSV) UL42  
XX protein, variola virus A10L protein, vaccinia virus virion core protein  
XX P4a, and human parainfluenza virus haemagglutinin-neuraminidase, where  
XX the contiguous amino acid sequence encompasses the YPXL motif of the viral  
XX protein. The peptides of the invention are useful in the manufacture of a  
XX medicament for treating viral infections caused by a virus selected from  
XX HCV, HSP-1 and variola virus. The peptides are also useful for inhibiting  
XX viral budding from virus-infected cells and/or inhibiting viral  
XX infectivity, thus inhibiting viral propagation in the cells. This  
XX sequence represents a Variola smallpox virus A10L YPXL motif containing  
XX peptide used in the treatment of viral infections of the invention.

XX Sequence 12 AA;

Query Match 44.4%; Score 28; DB 7; Length 12;  
Best Local Similarity 50.0%; Pred. No. 4e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERPDPENF 11  
:::| | | |

Db 2 KKKYDPLNF 9

RESULT 33  
ADCC44703  
ID ADCC44703 standard; peptide; 12 AA.  
XX

AC ADCC44703;

XX 18-DEC-2003 (first entry)

DE Endothelial cell binding peptide SEQ ID NO:432.

XX endothelial cell binding protein; EGBP; anti-tumour; cytostatic;

KM vasoactive; antiproliferative; dermatological; ophthalmological;

KM antidiabetic; antihypertensive; vulnary; antitumor; antiinflammatory;

XX antibacterial; gynaecological; angiogenesis.

OS Synthetic.

XX WO2003037172-A2.

PN 08-MAY-2003.

XX 01-NOV-2002; 2002WO-US035258.

XX 01-NOV-2001; 2001US-0334822P.

XX (GPCB-) GPC BIOTECH INC.

XX Gynaris J, Lamphere L, Morris AJ, Tsaioun K;

XX WPI; 2003-482072/45.

PS Claim 3; SEQ ID NO 432; 126pp; English.

XX The invention relates to a novel isolated, synthetic or recombinant

CC peptide or polypeptide which includes one or more endothelial cell

CC binding protein (EGBP) sequences. A peptide of the invention has anti-

CC tumour, cytostatic, vasoactive, antiproliferative, dermatological,

CC ophthalmological, antidiabetic, antihypertensive, vulnary, antitumor,

CC antiinflammatory, antibacterial, and gynaecological activity. The peptide

CC is useful for promoting, reducing the proliferation and/or migration of

CC endothelial cells, by treating the cells with an EGBP agonist, which is

CC preferably the peptide, to promote proliferation and/or migration of the

CC treated cells, and for reducing or promoting angiogenesis, by treating

CC the cells with an EGBP antagonist, which is preferably the peptide of the

CC invention. A peptide of the invention is also useful for manufacturing a

CC medicament for promoting angiogenesis, by admixing an EGBP agonist or

CC EGBP antagonist to promote or reduce angiogenesis at one or more sites in

CC a treated mammal. The medicament is useful for promoting or reducing

CC angiogenesis. EGBP sequences are useful to alter the infectivity spectrum

CC of a viral particle. The present sequence represents an EGBP of the

XX invention.

XX Sequence 12 AA;

XX

XX ADCC36084;  
AC  
XX 18-DEC-2003 (first entry)  
XX  
XX Chemokine binding peptide BKT-P125.

XX peptidic chemokine modulator; antiinflammatory; antiallergic;

KM immunosuppressive; antidiabetic; antirheumatic; dermatological;

KM antidiabetic; antibacterial; antiproliferative; antiseborrheic;

KM antidiabetic; antiproliferative; antiproliferative; antiproliferative;

KM antidiabetic; antiproliferative; antiproliferative; antiproliferative;

KM antidiabetic; antiproliferative; antiproliferative; antiproliferative;

KM antidiabetic; antiproliferative; antiproliferative; antiproliferative;

KM antidiabetic; antiproliferative; antiproliferative; antiproliferative;

KM antidiabetic; antiproliferative; antiproliferative; antiproliferative;

KM antidiabetic; antiproliferative; antiproliferative; antiproliferative;

KM antidiabetic; antiproliferative; antiproliferative; antiproliferative;

KM antidiabetic; antiproliferative; antiproliferative; antiproliferative;

KM antidiabetic; antiproliferative; antiproliferative; antiproliferative;

KM antidiabetic; antiproliferative; antiproliferative; antiproliferative;

KM antidiabetic; antiproliferative; antiproliferative; antiproliferative;

KM antidiabetic; antiproliferative; antiproliferative; antiproliferative;

KM antidiabetic; antiproliferative; antiproliferative; antiproliferative;

KM antidiabetic; antiproliferative; antiproliferative; antiproliferative;

KM antidiabetic; antiproliferative; antiproliferative; antiproliferative;

KM antidiabetic; antiproliferative; antiproliferative; antiproliferative;

KM antidiabetic; antiproliferative; antiproliferative; antiproliferative;

KM antidiabetic; antiproliferative; antiproliferative; antiproliferative;

KM antidiabetic; antiproliferative; antiproliferative; antiproliferative;

KM antidiabetic; antiproliferative; antiproliferative; antiproliferative;

KM antidiabetic; antiproliferative; antiproliferative; antiproliferative;

KM antidiabetic; antiproliferative; antiproliferative; antiproliferative;

KM antidiabetic; antiproliferative; antiproliferative; antiproliferative;

KM antidiabetic; antiproliferative; antiproliferative; antiproliferative;

KM antidiabetic; antiproliferative; antiproliferative; antiproliferative;

KM antidiabetic; antiproliferative; antiproliferative; antiproliferative;

KM antidiabetic; antiproliferative; antiproliferative; antiproliferative;

KM antidiabetic; antiproliferative; antiproliferative; antiproliferative;

KM antidiabetic; antiproliferative; antiproliferative; antiproliferative;

KM antidiabetic; antiproliferative; antiproliferative; antiproliferative;

KM antidiabetic; antiproliferative; antiproliferative; antiproliferative;

KM antidiabetic; antiproliferative; antiproliferative; antiproliferative;

XX Sequence 12 AA;

XX

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XX

XX The present invention describes a peptidic chemokine modulator (I) for

XX modulating a biological effect of a chemokine. (I) comprises a molecule

XX consisting of: (a) the amino acids His, Ser, Ala, Leu, Ile, Lys, Arg, Thr

XX and Pro, and features at least 2 histidines spread along the molecule, (b)

XX where the molecule features an overall positive charge (family 1); or (b)

XX the amino acids His, Pro, Thr, Leu, Arg and Tyr and features at least two

XX neighbouring histidines, where the molecule features an overall positive

XX charge (family 2). Also described: (1) a composition for treating a

XX condition involving abnormal cell migration in a subject; (2) a method

XX for treating a disease modulated through and/or caused by binding of a

XX chemokine to a chemokine receptor in a subject; (3) an antibody for

XX binding to a chemokine-binding receptor that recognises at least a

XX portion of a chemokine-binding receptor or the peptide; (4) a vaccine

XX formed with the antibody; and (5) a method for producing an antibody. (I)

XX has antiinflammatory, antiallergic, immunosuppressive, antidiabetic,

XX antirheumatic, dermatological, antidiabetic, antiproliferative,

XX antiproliferative, antiseborrheic, antidiabetic, antiproliferative,

XX antiproliferative, antiproliferative, antiproliferative, antiproliferative,

XX antiproliferative, antiproliferative, antiproliferative, antiproliferative,

XX antiproliferative, antiproliferative, antiproliferative, antiproliferative,

XX antiproliferative, antiproliferative, antiproliferative, antiproliferative,

XX antiproliferative, antiproliferative, antiproliferative, antiproliferative,

XX antiproliferative, antiproliferative, antiproliferative, antiproliferative,

XX antiproliferative, antiproliferative, antiproliferative, antiproliferative,

XX antiproliferative, antiproliferative, antiproliferative, antiproliferative,

XX antiproliferative, antiproliferative, antiproliferative, antiproliferative,

XX antiproliferative, antiproliferative, antiproliferative, antiproliferative,

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XX antiproliferative, antiproliferative, antiproliferative, antiproliferative,

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XX antiproliferative, antiproliferative, antiproliferative, antiproliferative,

XX antiproliferative, antiproliferative, antiproliferative, antiproliferative,

XX antiproliferative, antiproliferative, antiproliferative, antiproliferative;

XX Query Match 44.4%; Score 28; DB 7; Length 12;

XX Best Local Similarity 57.1%; Pred. No. 4e+02;

XX Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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XX RESULT 34

XX ADCC36084

XX ID ADCC36084 standard; peptide; 12 AA.

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Best Local Similarity 57.1%; Pred. No. 4e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 1; Mismatches 2;

OY 1 IYGERPP 7  
: ||| |  
Db 3 VYGNRLP 9

## RESULT 35

AAR46829  
ID AAR46829 standard; protein; 13 AA.

XX AAR46829;

DT 25-MAR-2003 (revised)  
DT 19-AUG-1994 (first entry)

XX pH 2.5 acid phosphatase derived peptide #816:5hphe.

XX pH 2.5; acid phosphatase; Trichoderma; host; Aspergillus; phytic acid;  
XX phytate degrading enzyme; PDE; removal; inositol hexaphosphoric acid;  
XX plant; feed composition; filtration.

XX Synthetic.

XX MO9403612-A1.

XX 17-FEB-1994.

XX 30-JUL-1993; 93WO-FI000310.

XX 31-JUL-1992; 92US-00923724.

XX (ALKO-) ALKO LTD.

XX Nevalainen HK, Palohelmo MT, Mattinen-Oinonen ASK, Torkkeli TK,  
PI Cantrell M, Piddington C, Rambosek JA, Turunen MK, Fagerstroem RB;

XX WPI, 1994-065700/08.

XX Compsns. cong. phytate degrading enzymes - obtd. by expression of their  
PI genes in Trichoderma, used patric. for producing animal feed compns.

XX Example 4; Page 46; 142pp; English.

XX The sequences given in AAR46825-35 are peptides derived from the pH2.5  
XX acid phosphatase protein. This phytase protein may be used in the  
XX composition of the invention. The DNA encoding the phytase protein may be  
XX introduced into a Trichoderma host which then expresses it and the  
XX protein is collected from the culture medium. By using Trichoderma as a  
XX host for Aspergillus phytate degrading enzymes such as this, a totally  
XX different enzyme composition compared to that secreted from Aspergillus  
XX results. The enzyme composition can be used for removal of phytic acid or  
XX inositol hexaphosphoric acid from raw material, particularly plant  
XX material. The composition is used in feed compositions for animals. By  
XX using Trichoderma as a source of a composition containing phytate  
XX degrading enzymes some difficult downstream processing problems, eg.  
XX filtration, that occur with similar Aspergillus compositions are avoided  
XX and yields are improved. (Updated on 25-MAR-2003 to correct FN field.)

XX Sequence 13 AA;

Query Match 44.4%; Score 28; DB 2; Length 13;

Best Local Similarity 66.7%; Pred. No. 4.4e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 2; Mismatches 0;

OY 2 YGERPP 7  
: ||| |  
Db 2 HGERYP 7

## RESULT 36

ADC43445

ID ADC43445 standard; peptide; 13 AA.

XX ADC43445;

DT 18-DEC-2003 (first entry)

DE Variola smallpox virus A10L YPXL motif containing peptide, SEQ ID NO 541.

XX viral; YPXL; cellular protein AP-50; hepatitis C virus; HCV;  
XX herpes simplex virus; HSV; UL42 protein; variola virus A10L;  
XX vaccinia virus vitron core protein P4a;  
XX human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;  
XX viral budding; viral infectivity.

XX Variola virus.

XX MO2003017943-A2.

XX 06-MAR-2003.

XX 22-AUG-2002; 2002MO-US027066.

XX 22-AUG-2001; 2001US-0314182P.

XX (MYRI-) MYRIAD GENETICS INC.

XX Morham S, Zavitz K, Hobden A;

XX WPI; 2003-371696/35.

XX Novel peptide, comprising a contiguous amino acid sequence of a viral  
PT protein, capable of binding to a region of cellular protein AP-50 is  
PT useful for treating viral infections.

XX Claim 31; SEQ ID NO 541; 60pp; English.

XX The invention relates to a novel isolated peptide comprising a contiguous  
XX amino acid sequence of 7-30 amino acid residues of a viral protein, where  
XX the contiguous amino acid sequence encompasses the YPXL motif of the  
XX viral protein, and the 7-30 amino acid residues 121-435 of cellular  
XX binding a region including the amino acid residues 121-435 of cellular  
XX protein AP-50. The isolated 7-30 amino acid viral protein is selected  
XX from hepatitis C virus (HCV) polypeptide, herpes simplex virus (HSV) UL42  
XX protein, variola virus A10L protein, vaccinia virus vitron core protein  
XX P4a, and human parainfluenza virus haemagglutinin-neuraminidase, where  
XX the contiguous amino acid sequence encompasses the YPXL motif of the viral  
XX protein. The peptides of the invention are useful in the manufacture of a  
XX medicament for treating viral infections caused by a virus selected from  
XX HCV, HSP-1 and variola virus. The peptides are also useful for inhibiting  
XX viral budding from virus-infected cells and/or inhibiting viral  
XX infectivity, thus inhibiting viral propagation in the cells. This  
XX sequence represents a Variola smallpox virus A10L YPXL motif containing  
XX peptide used in the treatment of viral infections of the invention.

XX Sequence 13 AA;

Query Match 44.4%; Score 28; DB 7; Length 13;

Best Local Similarity 50.0%; Pred. No. 4.4e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 3; Mismatches 1;

OY 4 ERFPDENF 11  
: ||| |  
Db 6 KKYVDLNF 13

## RESULT 37

ADC43424  
ID ADC43424 standard; peptide; 13 AA.

XX ADC43424;

DT 18-DEC-2003 (first entry)

DE Variola smallpox virus A10L YPXL motif containing peptide, SEQ ID No 520.  
XX  
KM viral; YPXL; cellular protein AP-50; hepatitis C virus; HCV;  
KM herpes simplex virus; HSV; UL42 protein; variola virus A10L;  
KM vaccinia virus virion core protein P4a;  
KM human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;  
KM viral budding; viral infectivity.  
OS  
XX Variola virus.  
XX  
XX WO2003017943-A2.  
XX  
XX PD 06-MAR-2003.  
XX  
XX PF 22-AUG-2002; 2002WO-US027066.  
XX  
XX PR 22-AUG-2001; 2001US-0314182P.  
XX  
XX PA (MYRI-) MYRIAD GENETICS INC.  
XX  
XX PI Morham S, Zavitz K, Hobden A;  
XX  
XX DR WPI; 2003-371696/35.  
XX  
PT Novel peptide, comprising a contiguous amino acid sequence of a viral  
PT protein, capable of binding to a region of cellular protein AP-50 is  
PT useful for treating viral infections.  
XX  
XX PS Claim 31; SEQ ID NO 520; 60bp; English.  
XX  
CC The invention relates to a novel isolated peptide comprising a contiguous  
CC amino acid sequence of 7-30 amino acid residues of a viral protein, where  
CC the contiguous amino acid sequence encompasses the YPXL motif of the  
CC viral protein, and the 7-30 amino acid viral protein is capable of  
CC binding a region including the amino acid residues 121-435 of cellular  
CC protein AP-50. The isolated 7-30 amino acid viral protein is selected  
CC from hepatitis C virus (HCV) polypeptide, herpes simplex virus (HSV) UL42  
CC protein, variola virus A10L protein, vaccinia virus virion core protein  
CC P4a, and human parainfluenza virus haemagglutinin-neuraminidase, where  
CC the contiguous amino acid sequence encompasses the YPXL motif of the viral  
CC protein. The peptides of the invention are useful in the manufacture of a  
CC medicament for treating viral infections caused by a virus selected from  
CC HCV, HSP-1 and variola virus. The peptides are also useful for inhibiting  
CC viral budding from virus-infected cells and/or inhibiting viral  
CC infectivity, thus inhibiting viral propagation in the cells. This  
CC sequence represents a Variola smallpox virus A10L YPXL motif containing  
CC peptide used in the treatment of viral infections of the invention.  
CC  
XX  
SQ Sequence 13 AA;  
Query Match 44.4%; Score 28; DB 7; Length 13;  
Best Local Similarity 50.0%; Pred. No. 4.4e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
QY 4 ERPDENF 11  
Db 4 KKYDPLNF 11  
ADCA3399  
ID ADCA3399 standard; peptide; 13 AA.  
XX  
XX AC ADCA3399;  
XX  
XX DT 18-DEC-2003 (first entry)  
XX  
DE Variola smallpox virus A10L YPXL motif containing peptide, SEQ ID No 495.  
XX  
XX KM viral; YPXL; cellular protein AP-50; hepatitis C virus; HCV;  
KM herpes simplex virus; HSV; UL42 protein; variola virus A10L;  
KM vaccinia virus virion core protein P4a;  
KM human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;  
XX

KM viral budding; viral infectivity.  
XX  
OS Variola virus.  
XX  
XX WO2003017943-A2.  
XX  
XX PD 06-MAR-2003.  
XX  
XX PF 22-AUG-2002; 2002WO-US027066.  
XX  
XX PR 22-AUG-2001; 2001US-0314182P.  
XX  
XX PA (MYRI-) MYRIAD GENETICS INC.  
XX  
XX PI Morham S, Zavitz K, Hobden A;  
XX  
XX DR WPI; 2003-371696/35.  
XX  
PT Novel peptide, comprising a contiguous amino acid sequence of a viral  
PT protein, capable of binding to a region of cellular protein AP-50 is  
PT useful for treating viral infections.  
XX  
XX PS Claim 31; SEQ ID NO 495; 60bp; English.  
XX  
CC The invention relates to a novel isolated peptide comprising a contiguous  
CC amino acid sequence of 7-30 amino acid residues of a viral protein, where  
CC the contiguous amino acid sequence encompasses the YPXL motif of the  
CC viral protein, and the 7-30 amino acid viral protein is capable of  
CC binding a region including the amino acid residues 121-435 of cellular  
CC protein AP-50. The isolated 7-30 amino acid viral protein is selected  
CC from hepatitis C virus (HCV) polypeptide, herpes simplex virus (HSV) UL42  
CC protein, variola virus A10L protein, vaccinia virus virion core protein  
CC P4a, and human parainfluenza virus haemagglutinin-neuraminidase, where  
CC the contiguous amino acid sequence encompasses the YPXL motif of the viral  
CC protein. The peptides of the invention are useful in the manufacture of a  
CC medicament for treating viral infections caused by a virus selected from  
CC HCV, HSP-1 and variola virus. The peptides are also useful for inhibiting  
CC viral budding from virus-infected cells and/or inhibiting viral  
CC infectivity, thus inhibiting viral propagation in the cells. This  
CC sequence represents a Variola smallpox virus A10L YPXL motif containing  
CC peptide used in the treatment of viral infections of the invention.  
CC  
XX  
SQ Sequence 13 AA;  
Query Match 44.4%; Score 28; DB 7; Length 13;  
Best Local Similarity 50.0%; Pred. No. 4.4e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
QY 4 ERPDENF 11  
Db 2 KKYDPLNF 9  
ADCA3412  
ID ADCA3412 standard; peptide; 13 AA.  
XX  
XX AC ADCA3412;  
XX  
XX DT 18-DEC-2003 (first entry)  
XX  
DE Variola smallpox virus A10L YPXL motif containing peptide, SEQ ID No 508.  
XX  
XX KM viral; YPXL; cellular protein AP-50; hepatitis C virus; HCV;  
KM herpes simplex virus; HSV; UL42 protein; variola virus A10L;  
KM vaccinia virus virion core protein P4a;  
KM human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;  
XX  
XX KM viral budding; viral infectivity.  
XX  
OS Variola virus.  
XX  
XX PN WO2003017943-A2.  
XX

PD 06-MAR-2003.  
XX  
XX 22-AUG-2002; 2002WO-US027066.  
XX  
XX 22-AUG-2001; 2001US-0314182P.  
XX  
XX (MYRI-) MYRIAD GENETICS INC.  
XX  
XX Morham S, Zavitz K, Hobden A;  
XX  
XX WPI; 2003-371696/35.  
XX  
XX Novel peptide, comprising a contiguous amino acid sequence of a viral  
PT protein, capable of binding to a region of cellular protein AP-50 is  
PT useful for treating viral infections.  
XX  
XX  
XX Claim 31; SEQ ID NO 508; 60pp; English.  
XX  
XX The invention relates to a novel isolated peptide comprising a contiguous  
CC amino acid sequence of 7-30 amino acid residues of a viral protein, where  
CC the contiguous amino acid sequence encompasses the YPXL motif of the  
CC viral protein, and the 7-30 amino acid residues 121-435 of cellular  
CC binding a region including the amino acid residues 121-435 of cellular  
CC protein AP-50. The isolated 7-30 amino acid viral protein is selected  
CC from hepatitis C virus (HCV) polypeptide, herpes simplex virus (HSV) UL42  
CC protein, varicella virus A10L protein, vaccinia virus virion core protein  
CC P4a, and human parainfluenza virus haemagglutinin-neuraminidase, where  
CC the contiguous amino acid sequence encompasses the YPXL motif of the viral  
CC protein. The peptides of the invention are useful in the manufacture of a  
CC medicament for treating viral infections caused by a virus selected from  
CC HCV, HSP-1 and varicella virus. The peptides are also useful for inhibiting  
CC viral budding from virus-infected cells and/or inhibiting viral  
CC infectivity, thus inhibiting viral propagation in the cells. This  
CC sequence represents a Varicella smallpox virus A10L YPXL motif containing  
CC peptide used in the treatment of viral infections of the invention.  
XX  
XX Sequence 13 AA;  
SQ  
Query Match 44.4%; Score 28; DB 7; Length 13;  
Best Local Similarity 50.0%; Pred. No. 4.4e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
QY 4 ERPDPENF 11  
: : : : :  
Db 3 KKPDPDNF 10  
RESULT 40  
ADCC43435  
ID ADCC43435 standard; peptide; 13 AA.  
XX  
XX ADCC43435;  
XX  
XX 18-DEC-2003 (first entry)  
XX  
XX Variola smallpox virus A10L YPXL motif containing peptide, SEQ ID NO 531.  
XX  
XX viral; YPXL; cellular protein AP-50; hepatitis C virus; HCV;  
XX herpes simplex virus; HSV; UL42 protein; varicella virus A10L;  
XX vaccinia virus virion core protein P4a;  
XX human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;  
XX viral budding; viral infectivity.  
XX  
XX Variola virus.  
XX  
XX WO2003017943-A2.  
XX  
XX 06-MAR-2003.  
XX  
XX 22-AUG-2002; 2002WO-US027066.  
XX  
XX 22-AUG-2001; 2001US-0314182P.  
XX  
XX WPI; 2003-371696/35.  
XX

PA (MYRI-) MYRIAD GENETICS INC.  
XX  
XX Morham S, Zavitz K, Hobden A;  
XX  
XX WPI; 2003-371696/35.  
XX  
XX Novel peptide, comprising a contiguous amino acid sequence of a viral  
PT protein, capable of binding to a region of cellular protein AP-50 is  
PT useful for treating viral infections.  
XX  
XX  
XX Claim 31; SEQ ID NO 531; 60pp; English.  
XX  
XX The invention relates to a novel isolated peptide comprising a contiguous  
CC amino acid sequence of 7-30 amino acid residues of a viral protein, where  
CC the contiguous amino acid sequence encompasses the YPXL motif of the  
CC viral protein, and the 7-30 amino acid residues 121-435 of cellular  
CC binding a region including the amino acid residues 121-435 of cellular  
CC protein AP-50. The isolated 7-30 amino acid viral protein is selected  
CC from hepatitis C virus (HCV) polypeptide, herpes simplex virus (HSV) UL42  
CC protein, varicella virus A10L protein, vaccinia virus virion core protein  
CC P4a, and human parainfluenza virus haemagglutinin-neuraminidase, where  
CC the contiguous amino acid sequence encompasses the YPXL motif of the viral  
CC protein. The peptides of the invention are useful in the manufacture of a  
CC medicament for treating viral infections caused by a virus selected from  
CC HCV, HSP-1 and varicella virus. The peptides are also useful for inhibiting  
CC viral budding from virus-infected cells and/or inhibiting viral  
CC infectivity, thus inhibiting viral propagation in the cells. This  
CC sequence represents a Varicella smallpox virus A10L YPXL motif containing  
CC peptide used in the treatment of viral infections of the invention.  
XX  
XX Sequence 13 AA;  
SQ  
Query Match 44.4%; Score 28; DB 7; Length 13;  
Best Local Similarity 50.0%; Pred. No. 4.4e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
QY 4 ERPDPENF 11  
: : : : :  
Db 5 KKPDPDNF 12  
RESULT 41  
ADCC43386  
ID ADCC43386 standard; peptide; 13 AA.  
XX  
XX ADCC43386;  
XX  
XX 18-DEC-2003 (first entry)  
XX  
XX Variola smallpox virus A10L YPXL motif containing peptide, SEQ ID NO 482.  
XX  
XX viral; YPXL; cellular protein AP-50; hepatitis C virus; HCV;  
XX herpes simplex virus; HSV; UL42 protein; varicella virus A10L;  
XX vaccinia virus virion core protein P4a;  
XX human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;  
XX viral budding; viral infectivity.  
XX  
XX Variola virus.  
XX  
XX WO2003017943-A2.  
XX  
XX 06-MAR-2003.  
XX  
XX 22-AUG-2002; 2002WO-US027066.  
XX  
XX 22-AUG-2001; 2001US-0314182P.  
XX  
XX (MYRI-) MYRIAD GENETICS INC.  
XX  
XX Morham S, Zavitz K, Hobden A;  
XX  
XX WPI; 2003-371696/35.  
XX

PT Novel peptide, comprising a contiguous amino acid sequence of a viral  
PT protein, capable of binding to a region of cellular protein AP-50 is  
PT useful for treating viral infections.

PS Claim 31; SEQ ID NO 482; 60pp; English.

CC The invention relates to a novel isolated peptide comprising a contiguous  
CC amino acid sequence of 7-30 amino acid residues of a viral protein, where  
CC the contiguous amino acid sequence encompasses the YPXL motif of the  
CC viral protein, and the 7-30 amino acid residues is capable of  
CC binding a region including the amino acid residues 121-435 of cellular  
CC protein AP-50. The isolated 7-30 amino acid viral protein is selected  
CC from hepatitis C virus (HCV) polypeptide, herpes simplex virus (HSV) UL42  
CC protein, varicella virus A10L protein, vaccinia virus virion core protein  
CC P4a, and human parainfluenza virus haemagglutinin-neuraminidase, where  
CC the contiguous amino acid sequence encompasses the YPXL motif of the viral  
CC protein. The peptides of the invention are useful in the manufacture of a  
CC medicament for treating viral infections caused by a virus selected from  
CC HCV, HSP-1 and varicella virus. The peptides are also useful for inhibiting  
CC viral budding from virus-infected cells and/or inhibiting viral  
CC infectivity, thus inhibiting viral propagation in the cells. This  
CC sequence represents a varicella smallpox virus A10L YPXL motif containing  
CC peptide used in the treatment of viral infections of the invention.

CC Sequence 13 AA;

Query Match 44.4%; Score 28; DB 7; Length 13;  
Best Local Similarity 50.0%; Pred. No. 4.4e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPDENF 11  
:::| | | |  
DB 1 KKYDPLNF 8

RESULT 42

ADC43436  
ID ADC43436 standard; peptide; 14 AA.

AC ADC43436;

DT 18-DEC-2003 (first entry)

DE Variola smallpox virus A10L YPXL motif containing peptide, SEQ ID NO 532.

KM viral; YPXL; cellular protein AP-50; hepatitis C virus; HCV;  
KM herpes simplex virus; HSV; UL42 protein; varicella virus A10L;  
KM vaccinia virus virion core protein P4a;  
KM human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;  
KM viral budding; viral infectivity.

OS Variola virus.

PN WO2003017943-A2.

PD 06-MAR-2003.

PF 22-AUG-2002; 2002WO-US027066.

PR 22-AUG-2001; 2001US-0314182P.

PA (MYRI-) MYRIAD GENETICS INC.

PI Morham S, Zavitz K, Hobden A;

WPI; 2003-371696/35.

Novel peptide, comprising a contiguous amino acid sequence of a viral  
PT protein, capable of binding to a region of cellular protein AP-50 is  
PT useful for treating viral infections.

Claim 31; SEQ ID NO 532; 60pp; English.

CC The invention relates to a novel isolated peptide comprising a contiguous  
CC amino acid sequence of 7-30 amino acid residues of a viral protein, where  
CC the contiguous amino acid sequence encompasses the YPXL motif of the  
CC viral protein, and the 7-30 amino acid residues is capable of  
CC binding a region including the amino acid residues 121-435 of cellular  
CC protein AP-50. The isolated 7-30 amino acid viral protein is selected  
CC from hepatitis C virus (HCV) polypeptide, herpes simplex virus (HSV) UL42  
CC protein, varicella virus A10L protein, vaccinia virus virion core protein  
CC P4a, and human parainfluenza virus haemagglutinin-neuraminidase, where  
CC the contiguous amino acid sequence encompasses the YPXL motif of the viral  
CC protein. The peptides of the invention are useful in the manufacture of a  
CC medicament for treating viral infections caused by a virus selected from  
CC HCV, HSP-1 and varicella virus. The peptides are also useful for inhibiting  
CC viral budding from virus-infected cells and/or inhibiting viral  
CC infectivity, thus inhibiting viral propagation in the cells. This  
CC sequence represents a varicella smallpox virus A10L YPXL motif containing  
CC peptide used in the treatment of viral infections of the invention.

CC Sequence 14 AA;

Query Match 44.4%; Score 28; DB 7; Length 14;  
Best Local Similarity 50.0%; Pred. No. 4.7e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPDENF 11  
:::| | | |  
DB 5 KKYDPLNF 12

RESULT 43

ADC43387  
ID ADC43387 standard; peptide; 14 AA.

AC ADC43387;

DT 18-DEC-2003 (first entry)

DE Variola smallpox virus A10L YPXL motif containing peptide, SEQ ID NO 483.

KM viral; YPXL; cellular protein AP-50; hepatitis C virus; HCV;  
KM herpes simplex virus; HSV; UL42 protein; varicella virus A10L;  
KM vaccinia virus virion core protein P4a;  
KM human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;  
KM viral budding; viral infectivity.

OS Variola virus.

PN WO2003017943-A2.

PD 06-MAR-2003.

PF 22-AUG-2002; 2002WO-US027066.

PR 22-AUG-2001; 2001US-0314182P.

PA (MYRI-) MYRIAD GENETICS INC.

PI Morham S, Zavitz K, Hobden A;

WPI; 2003-371696/35.

Novel peptide, comprising a contiguous amino acid sequence of a viral  
PT protein, capable of binding to a region of cellular protein AP-50 is  
PT useful for treating viral infections.

Claim 31; SEQ ID NO 483; 60pp; English.

CC The invention relates to a novel isolated peptide comprising a contiguous  
CC amino acid sequence of 7-30 amino acid residues of a viral protein, where  
CC the contiguous amino acid sequence encompasses the YPXL motif of the  
CC viral protein, and the 7-30 amino acid residues is capable of  
CC binding a region including the amino acid residues 121-435 of cellular  
CC protein AP-50. The isolated 7-30 amino acid viral protein is selected



CC from hepatitis C virus (HCV) polyprotein, herpes simplex virus (HSV) UL42  
CC protein, variola virus A10L protein, vaccinia virus virion core protein  
CC P44, and human parainfluenza virus haemagglutinin-neuraminidase, where  
CC the contiguous amino acid sequence encompasses the YPKL motif of the viral  
CC protein. The peptides of the invention are useful in the manufacture of a  
CC medicament for treating viral infections caused by a virus selected from  
CC HCV, HSP-1 and variola virus. The peptides are also useful for inhibiting  
CC viral budding from virus-infected cells and/or inhibiting viral  
CC infectivity, thus inhibiting viral propagation in the cells. This  
CC sequence represents a Variola smallpox virus A10L YPKL motif containing  
CC peptide used in the treatment of viral infections of the invention.

XX Sequence 14 AA;

Query Match 44.4%; Score 28; DB 7; Length 14;  
Best Local Similarity 50.0%; Pred. No. 4.7e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPDENF 11  
Db 1 KKYPDLNF 8

RESULT 44

ID ADC43413 standard; peptide; 14 AA.

XX ADC43413;

DT 18-DEC-2003 (first entry)

DE Variola smallpox virus A10L YPKL motif containing peptide, SEQ ID No 509.

XX viral; YPKL; cellular protein AP-50; hepatitis C virus; HCV;  
KM herpes simplex virus; HSV; UL42 protein; variola virus A10L;  
KM vaccinia virus virion core protein P44;  
KM human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;  
KM viral budding; viral infectivity.

XX Variola virus.

OS WO2003017943-A2.

XX 06-MAR-2003.

PF 22-AUG-2002; 2002MO-US027066.

PR 22-AUG-2001; 2001US-0314182P.

XX (MYRI-) MYRIAD GENETICS INC.

PI Morham S, Zavitz K, Hobden A;

XX WPI; 2003-371696/35.

DR Novel peptide, comprising a contiguous amino acid sequence of a viral  
XX protein, capable of binding to a region of cellular protein AP-50 is  
XX useful for treating viral infections.

XX Claim 31; SEQ ID NO 509; 60pp; English.

XX The invention relates to a novel isolated peptide comprising a contiguous  
XX amino acid sequence of 7-30 amino acid residues of a viral protein, where  
XX the contiguous amino acid sequence encompasses the YPKL motif of the  
XX viral protein, and the 7-30 amino acid viral protein is capable of  
XX binding a region including the amino acid residues 121-435 of cellular  
XX protein AP-50. The isolated 7-30 amino acid viral protein is selected  
XX from hepatitis C virus (HCV) polyprotein, herpes simplex virus (HSV) UL42  
XX protein, variola virus A10L protein, vaccinia virus virion core protein  
XX P44, and human parainfluenza virus haemagglutinin-neuraminidase, where  
XX the contiguous amino acid sequence encompasses the YPKL motif of the viral  
XX protein. The peptides of the invention are useful in the manufacture of a  
XX medicament for treating viral infections caused by a virus selected from

CC HCV, HSP-1 and variola virus. The peptides are also useful for inhibiting  
CC viral budding from virus-infected cells and/or inhibiting viral  
CC infectivity, thus inhibiting viral propagation in the cells. This  
CC sequence represents a Variola smallpox virus A10L YPKL motif containing  
CC peptide used in the treatment of viral infections of the invention.

XX Sequence 14 AA;

Query Match 44.4%; Score 28; DB 7; Length 14;  
Best Local Similarity 50.0%; Pred. No. 4.7e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPDENF 11  
Db 3 KKYPDLNF 10

RESULT 45

ID ADC43425 standard; peptide; 14 AA.

XX ADC43425;

DT 18-DEC-2003 (first entry)

DE Variola smallpox virus A10L YPKL motif containing peptide, SEQ ID No 521.

XX viral; YPKL; cellular protein AP-50; hepatitis C virus; HCV;  
KM herpes simplex virus; HSV; UL42 protein; variola virus A10L;  
KM vaccinia virus virion core protein P44;  
KM human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;  
KM viral budding; viral infectivity.

XX Variola virus.

OS WO2003017943-A2.

XX 06-MAR-2003.

PF 22-AUG-2002; 2002MO-US027066.

PR 22-AUG-2001; 2001US-0314182P.

XX (MYRI-) MYRIAD GENETICS INC.

PI Morham S, Zavitz K, Hobden A;

XX WPI; 2003-371696/35.

DR Novel peptide, comprising a contiguous amino acid sequence of a viral  
XX protein, capable of binding to a region of cellular protein AP-50 is  
XX useful for treating viral infections.

XX Claim 31; SEQ ID NO 521; 60pp; English.

XX The invention relates to a novel isolated peptide comprising a contiguous  
XX amino acid sequence of 7-30 amino acid residues of a viral protein, where  
XX the contiguous amino acid sequence encompasses the YPKL motif of the  
XX viral protein, and the 7-30 amino acid viral protein is capable of  
XX binding a region including the amino acid residues 121-435 of cellular  
XX protein AP-50. The isolated 7-30 amino acid viral protein is selected  
XX from hepatitis C virus (HCV) polyprotein, herpes simplex virus (HSV) UL42  
XX protein, variola virus A10L protein, vaccinia virus virion core protein  
XX P44, and human parainfluenza virus haemagglutinin-neuraminidase, where  
XX the contiguous amino acid sequence encompasses the YPKL motif of the viral  
XX protein. The peptides of the invention are useful in the manufacture of a  
XX medicament for treating viral infections caused by a virus selected from  
XX HCV, HSP-1 and variola virus. The peptides are also useful for inhibiting  
XX viral budding from virus-infected cells and/or inhibiting viral  
XX infectivity, thus inhibiting viral propagation in the cells. This  
XX sequence represents a Variola smallpox virus A10L YPKL motif containing  
XX peptide used in the treatment of viral infections of the invention.

SQ Sequence 14 AA;

Query Match 44.4%; Score 28; DB 7; Length 14;  
 Best Local Similarity 50.0%; Pred. No. 4.7e+02;  
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 4 ERPPDENF 11  
 : : : : :  
 Db 4 KRIPLDLP 11

Search completed: August 30, 2004, 10:49:33  
 Job time : 18.385 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:34 ; Search time 8.66554 Seconds

(without alignments)  
327.696 Million cell updates/sec

Title: US-09-720-469A-7  
Sequence: 1 RPPDENPKL 9

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 3347

Minimum DB seq length: 8  
Maximum DB seq length: 14

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25: \*  
1: sp\_archaea: \*  
2: sp\_bacteria: \*  
3: sp\_fungi: \*  
4: sp\_human: \*  
5: sp\_invertebrate: \*  
6: sp\_mammal: \*  
7: sp\_muc: \*  
8: sp\_organelle: \*  
9: sp\_phage: \*  
10: sp\_plant: \*  
11: sp\_rodent: \*  
12: sp\_virus: \*  
13: sp\_vertebrate: \*  
14: sp\_unclassified: \*  
15: sp\_virus: \*  
16: sp\_bacteriap: \*  
17: sp\_archaeap: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	46.0	13	Q9UP67	Q9UP67 homo sapien
2	24	46.0	10	P96352	P96352 marincbacte
3	23	46.0	10	Q931E5	Q931E5 photobacte
4	23	46.0	10	P96321	P96321 escherichia
5	23	46.0	10	P96306	P96306 aeromonas s
6	23	46.0	14	P96350	P96350 legionella
7	21	42.0	10	P96305	P96305 alteromonas
8	20	40.0	10	P96423	P96423 pseudomonas
9	20	40.0	13	Q8WY56	Q8WY56 homo sapien
10	20	40.0	14	Q45876	Q45876 clostridium
11	20	40.0	14	Q45872	Q45872 clostridium
12	19	38.0	10	Q9UCR0	Q9UCR0 homo sapien
13	18	36.0	10	Q725A2	Q725A2 homo sapien
14	18	36.0	10	Q9QV67	Q9QV67 rattus norv
15	18	36.0	10	Q63389	Q63389 rattus norv
16	18	36.0	11	Q9D232	Q9D232 human immun

17	18	36.0	13	Q9UNV6	Q9UNV6 homo sapien
18	18	36.0	14	Q52840	Q52840 rhizobium 1
19	18	36.0	14	Q52636	Q52636 escherichia
20	17	34.0	8	Q7X139	Q7X139 staphylococ
21	17	34.0	10	P96421	P96421 neisseria g
22	17	34.0	11	Q9A1Z8	Q9A1Z8 carsonella
23	17	34.0	12	Q9TWV4	Q9TWV4 lymnaea stea
24	17	34.0	14	Q9RSR5	Q9RSR5 staphylococ
25	17	34.0	14	P78359	P78359 homo sapien
26	17	34.0	14	Q9JUT5	Q9JUT5 mus musculu
27	16	32.0	9	Q93LE4	Q93LE4 heliobacill
28	16	32.0	11	Q47604	Q47604 escherichia
29	16	32.0	12	Q81VH0	Q81VH0 homo sapien
30	16	32.0	12	Q88577	Q88577 theiler's e
31	16	32.0	12	Q88578	Q88578 theiler's e
32	16	32.0	12	Q88579	Q88579 theiler's e
33	16	32.0	12	Q88575	Q88575 theiler's e
34	16	32.0	12	Q88580	Q88580 theiler's e
35	16	32.0	12	Q88582	Q88582 theiler's e
36	16	32.0	12	Q88581	Q88581 theiler's e
37	16	32.0	12	Q88576	Q88576 theiler's e
38	16	32.0	13	Q865C9	Q865C9 sus scrofa
39	16	32.0	13	Q85L68	Q85L68 monacthes a
40	16	32.0	13	Q83171	Q83171 cauliflower
41	16	32.0	13	Q83172	Q83172 ficedula al
42	16	32.0	14	Q55326	Q55326 synchococc
43	16	32.0	14	Q8V306	Q8V306 tomato yell
44	15	30.0	8	P72279	P72279 rhodococcus
45	15	30.0	13	Q7T282	Q7T282 geochelone

#### ALIGNMENTS

RESULT 1  
ID Q9UP67 PRELIMINARY; PRT; 13 AA.

AC Q9UP67;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Icosine monophosphatase 2 (Fragment).  
GN IMPA2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP MEDLINE=97463449; PubMed=9322233;  
RX Yoshikawa T., Turner G., Esterling L.E., Sanders A.R.,  
RA Defera-Wadleigh S.D.;  
RT "A novel human myo-inositol monophosphatase gene, IMP.18p, maps to a  
susceptibility region for bipolar disorder.";  
RL Mol. Psychiatry 2:393-397(1997).  
RN [2]  
RP MEDLINE=20264187;  
RX Yoshikawa T., Padigaru M., Karkera J.D., Sharma M., Berrettini W.H.,  
RA Esterling L.E., Defera-Wadleigh S.D.;  
RT "Genomic structure and novel variants of myo-inositol monophosphatase  
2.";  
RL Mol. Psychiatry 5:165-171(2000).  
DR EMBL; AF025882; AAD2236.1; -.  
DR EMBL; AF025881; AAD2236.1; JOINED.  
FT NON\_TER  
FT SEQUENCE 13 AA; 1589 MW; F3415D841F48D401 CR664;  
SQ

Query Match 48.0%; Score 24; DB 4; Length 13;  
Best Local Similarity 57.1%; Pred. No. 8.6e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 REPDEFN 7  
Db 2 RPSHRF 8

## RESULT 2

ID P96352 PRELIMINARY; PRT; 10 AA.

AC P96352;  
DT 01-MAY-1997 (TREMBlrel. 03, Created)  
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)  
DT 01-MAY-2001 (TREMBlrel. 16, Last annotation update)  
DE Coded portion of proteolysis tag (Fragment).  
OS Marinobacter hydrocarbonoclasticus (Pseudomonas nautical).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;  
OC Alteromonadaceae; Marinobacter.  
OX NCBI\_Taxid=2743;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 49840;  
RX MEDLINE=97128184; PubMed=8972778;  
RA Williams K.P.; Bartel D.P.;  
RT "Phylogenetic analysis of tmRNA secondary structure."  
RL RNA 2:1306-1310(1996).  
DR EMBL; U68077; AAB48027.1; -.  
FT NON TER 1  
SQ SEQUENCE 10 AA; 1051 MW; 857BD22DCB544B1A CRC64;

Query Match 46.0%; Score 23; DB 2; Length 10;  
Best Local Similarity 66.7%; Pred. No. 1e+03;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 DENFKL 9  
Db 3 DENYAL 8

RESULT 3  
ID Q93LE5 PRELIMINARY; PRT; 10 AA.

AC Q93LE5;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE Proteolysis tag (Fragment).  
OS Photobacterium phosphoreum.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
OC Vibrionaceae; Photobacterium.  
OX NCBI\_Taxid=659;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20063247; PubMed=10592213;  
RA Williams K.P.;  
RT "The tmRNA website."  
RL Nucleic Acids Res. 28:168-168(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Williams K.P.;  
RT "Phylogenetic analysis of tmRNA."  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY040837; AAK83525.1; -.  
FT NON TER 1  
SQ SEQUENCE 10 AA; 1051 MW; 857BD22DCB544B1A CRC64;

Query Match 46.0%; Score 23; DB 2; Length 10;  
Best Local Similarity 66.7%; Pred. No. 1e+03;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 DENFKL 9  
Db 3 DENYAL 8

RESULT 4  
ID P96321 PRELIMINARY; PRT; 10 AA.

AC P96321;  
DT 01-MAY-1997 (TREMBlrel. 03, Created)  
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)  
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)  
DE Coded portion of proteolysis tag (Fragment).  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_Taxid=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 133;  
RX MEDLINE=95023883; PubMed=7524073;  
RA Komine Y.; Kitabatake M.; Yokogawa T.; Nishikawa K.; Inokuchi H.;  
RT "A tRNA-like structure is present in 10Sa RNA, a small stable RNA from Escherichia coli."  
RL Proc. Natl. Acad. Sci. U.S.A. 91:9223-9227(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 133;  
RX MEDLINE=97128184; PubMed=8972778;  
RA Williams K.P.; Bartel D.P.;  
RT "Phylogenetic analysis of tmRNA secondary structure."  
RL RNA 2:1306-1310(1996).  
DR EMBL; U68074; AAB48024.1; -.  
FT NON TER 1  
SQ SEQUENCE 10 AA; 1051 MW; 857BD22DCB544B1A CRC64;

Query Match 46.0%; Score 23; DB 2; Length 10;  
Best Local Similarity 66.7%; Pred. No. 1e+03;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 DENFKL 9  
Db 3 DENYAL 8

RESULT 5  
ID P96306 PRELIMINARY; PRT; 10 AA.

AC P96306;  
DT 01-MAY-1997 (TREMBlrel. 03, Created)  
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)  
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)  
DE Coded portion of proteolysis tag (Fragment).  
OS Aeromonas salmonicida.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;  
OC Aeromonadaceae; Aeromonas.  
OX NCBI\_Taxid=645;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 33658;  
RX MEDLINE=97128184; PubMed=8972778;  
RA Williams K.P.; Bartel D.P.;  
RT "Phylogenetic analysis of tmRNA secondary structure."  
RL RNA 2:1306-1310(1996).  
DR EMBL; U68075; AAB48022.1; -.  
FT NON TER 1  
SQ SEQUENCE 10 AA; 1051 MW; 857BD22DCB544B1A CRC64;

Query Match 46.0%; Score 23; DB 2; Length 10;  
Best Local Similarity 66.7%; Pred. No. 1e+03;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 DENFKL 9  
Db 3 DENYAL 8

## RESULT 6

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P96350
ID P96350 PRELIMINARY; PRT; 14 AA.
AC P96350;
DT 01-MAY-1997 (TREMblrel. 03, Created)
DT 01-MAY-1997 (TREMblrel. 03, Last sequence update)
DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)
DE Coded portion of proteolysis tag (Fragment).
OS Legionella pneumophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=446;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33152;
RX MEDLINE=97128184; PubMed=8972778;
RA Williams K.P., Bartel D.P.;
RT "Phylogenetic analysis of tmRNA secondary structure.";
RL RNA 2:1306-1310(1996).
DR EMBL; U68079; AAB48026.1; -.
FT NON TER 1
SQ SEQUENCE 14 AA; 1349 MW; CEF5F7318D3B7D7D CRC64;

Query Match 46.0%; Score 23; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DENFKL 7
DB 3 DENVL 6

RESULT 7
P96305 PRELIMINARY; PRT; 10 AA.
ID P96305;
AC P96305;
DT 01-MAY-1997 (TREMblrel. 03, Created)
DT 01-MAY-1997 (TREMblrel. 03, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Coded portion of proteolysis tag (Fragment).
OS Alteromonas haloplanktis (Pseudalteromonas haloplanktis).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Alteromonadaceae; Pseudalteromonas.
OX NCBI_TaxID=228;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 14393;
RX MEDLINE=97128184; PubMed=8972778;
RA Williams K.P., Bartel D.P.;
RT "Phylogenetic analysis of tmRNA secondary structure.";
RL RNA 2:1306-1310(1996).
DR EMBL; U68076; AAB48021.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1053 MW; 857BD235AB544AAA CRC64;

Query Match 42.0%; Score 21; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 DENFKL 9
DB 3 DENVSL 8

RESULT 8
P96423 PRELIMINARY; PRT; 10 AA.
ID P96423;
AC P96423;
DT 01-MAY-1997 (TREMblrel. 03, Created)
DT 01-MAY-1997 (TREMblrel. 03, Last sequence update)
DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
DE Coded portion of proteolysis tag (Translated portion of tmRNA gene
DE ssa) (Fragment).
GN PA0826.1.

```

```

OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 25330;
RX MEDLINE=97128184; PubMed=8972778;
RA Williams K.P., Bartel D.P.;
RT "Phylogenetic analysis of tmRNA secondary structure.";
RL RNA 2:1306-1310(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Madman S., Yuan Y.,
RA Brody L.U., Coulter S.N., Polger K.R., Kas A., Lartig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Dory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL; U68078; AAB48029.1; -.
DR EMBL; AE004517; AA042616.1; -.
KW Complete proteome.
FT NON TER 1
SQ SEQUENCE 10 AA; 1037 MW; 857BD22DCB544AAA CRC64;

Query Match 40.0%; Score 20; DB 16; Length 10;
Best Local Similarity 50.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 DENFKL 9
DB 3 DENVSL 8

RESULT 9
Q8WY56 PRELIMINARY; PRT; 13 AA.
ID Q8WY56;
AC Q8WY56;
DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
DE Epithelial sodium channel beta-3 subunit (Fragment).
OS SCNN1B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Thomas C.P., Loftus R.W., Liu K.Z., Itani O.A.;
RT "Genomic organization of the 5' end of human beta ENaC and preliminary
RT characterization of its promoter.";
RL Am. J. Physiol. Renal Physiol. 0:0-0(2002).
DR EMBL; AF260228; AL48197.1; -.
DR GO; GO:0005216; F:ion channel activity; IEA.
KW Ionic channel.
FT NON TER 13
SQ SEQUENCE 13 AA; 1437 MW; 1716D00275917724 CRC64;

Query Match 40.0%; Score 20; DB 4; Length 13;
Best Local Similarity 60.0%; Pred. No. 5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 DENFKL 8
DB 9 DKNFQ 13

```

RESULT 10  
 ID Q45876 PRELIMINARY; PRT; 14 AA.  
 AC Q45876;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE HA-II protein (Fragment).  
 GN HA-II  
 OS Clostridium botulinum.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium.  
 OX NCBI\_TaxID=1491;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NCTC 7273;  
 RA East A.K., Stacey J.M., Collins M.D.;  
 RT "Cloning and sequencing of a hemagglutinin component of the botulinum  
 neurotoxin complex encoded by Clostridium botulinum types A and B.";  
 RL Syst. Appl. Microbiol. 17:306-312(1994).  
 DR EMBL; X79102; CAAS5711.1; -;  
 DR PIR; S58866; S58866.  
 DR InterPro: IPR008903; Botulinum\_HA-17.  
 DR Pfam: PF05588; botulinum\_HA-17; 1.  
 FT NON\_TER 14  
 SQ SEQUENCE 14 AA; 1628 MW; CD689B0937D75E29 CRC64;  
 Query Match 40.0%; Score 20; DB 2; Length 14;  
 Best Local Similarity 50.0%; Pred. No. 5.4e+03;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

RESULT 11  
 ID Q45872 PRELIMINARY; PRT; 14 AA.  
 AC Q45872; Q45869;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE (NCTC 7272 type A) HA-33 and P-21 genes (Fragment).  
 GN HA-II.  
 OS Clostridium botulinum.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium.  
 OX NCBI\_TaxID=1491;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NCTC 7272, TYPE A, and 17B;  
 RA East A.K., Stacey J.M., Collins M.D.;  
 RL Syst. Appl. Microbiol. 17:306-312(1994).  
 DR EMBL; X79104; CAAS5719.1; -;  
 DR EMBL; X79103; CAAS5715.1; -;  
 DR PIR; S58862; S58862.  
 DR InterPro: IPR008903; Botulinum\_HA-17.  
 DR Pfam: PF05588; botulinum\_HA-17; 1.  
 FT NON\_TER 14  
 SQ SEQUENCE 14 AA; 1656 MW; CD689B1BCD75E29 CRC64;  
 Query Match 40.0%; Score 20; DB 2; Length 14;  
 Best Local Similarity 50.0%; Pred. No. 5.4e+03;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

RESULT 12  
 Q9UCRO

ID Q9UCRO PRELIMINARY; PRT; 10 AA.  
 AC Q9UCRO;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE AUTOTAXIN (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92129337; PubMed=1739349;  
 RA Stracke M.L., Knutson H.C., Unsworth E.J., Arrestad A., Cioce V.,  
 RA Schiffmann E., Liotta L.A.;  
 RT "Identification, purification, and partial sequence analysis of  
 RT autotaxin, a novel motility-stimulating protein.";  
 RL J. Biol. Chem. 267:2524-2529(1992).  
 DR J. Biol. Chem. 267:2524-2529(1992).  
 DR GO; GO:0005576; Cytoplasmic; IDA.  
 DR GO; GO:0030334; P:regulation of cell migration; IDA.  
 FT NON\_TER 1  
 SQ SEQUENCE 10 AA; 1193 MW; 3501FB40544B19D7 CRC64;  
 Query Match 38.0%; Score 19; DB 4; Length 10;  
 Best Local Similarity 57.1%; Pred. No. 6e+03;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 13  
 ID Q725A2 PRELIMINARY; PRT; 10 AA.  
 AC Q725A2;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC Tissue=Testis;  
 RA Fraisl P., Forss-Petter S., Berger J.;  
 RT "A novel relative of Bubblegum.";  
 RT Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; A0577571; CAEL2153.1; -;  
 KW Hypothetical protein.  
 SQ SEQUENCE 10 AA; 1086 MW; 622094D8786769D4 CRC64;  
 Query Match 36.0%; Score 18; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 14  
 ID Q9QVF7 PRELIMINARY; PRT; 10 AA.  
 AC Q9QVF7;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Beta 2-glycoprotein I, beta 2-GPI (Fragment).  
 OS Rattus sp.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10118;  
RN [1]  
RP SEQUENCE  
RX MEDLINE=92135065; PubMed=1777418;  
RA Matsura E., Igatah M., Igatah Y., Nagae H., Ichikawa K.,  
RA Yasuda T., Koike T.;  
RT "Molecular definition of human beta 2-glycoprotein I (beta 2-GPI) by  
RT cDNA cloning and inter-species differences of beta 2-GPI in  
RT alternation of anticardiolipin binding.";  
RL Int. Immunol. 3:1217-1221(1991).  
FT NON\_TER 1  
FT NON\_TER 10  
SQ SEQUENCE 10 AA; 1100 MW; 94E681B767376E8A1 CRC64;

Query Match 36.0%; Score 18; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred. No. 9.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDE 5  
Db 7 PDE 9

RESULT 15  
Q63389 PRELIMINARY; PRT; 10 AA.  
AC Q63389;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE Ornithine decarboxylase (ODC).  
DB Rattus norvegicus (Rat).\_  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley; TISSUE=Testis;  
RX MEDLINE=89255378; PubMed=2722815;  
RA Wen L., Huang J.K., Blackshear P.J.;  
RT "Rat ornithine decarboxylase gene. Nucleotide sequence, potential  
RT regulatory elements, and comparison to the mouse gene.";  
RL J. Biol. Chem. 264:9016-9021(1989).  
DR EMBL; J04791; AA86163.1; -.  
DR PIR; B33710; B33710.  
SQ SEQUENCE 10 AA; 1074 MW; 30F6EE69D415BDC7 CRC64;

Query Match 36.0%; Score 18; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred. No. 9.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFP 3  
Db 6 RFP 8

RESULT 16  
Q9DZ32 PRELIMINARY; PRT; 11 AA.  
AC Q9DZ32;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
DE Gag polypeptide (Fragment).  
GN GAG.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroviridae; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20461476; PubMed=11005867;

RA Martinez-Picado J., DePasquale M.P., Kartsonis N., Hanna G.J.,  
RA Wong J., Finzi D., Rosenberg B., Gurchard H.F., Sutton L., Savara A.,  
RA Petropoulos C.J., Hellmann N., Walker B.D., Richman D.D.,  
RA Siliciano R., D'Agula R.T.;  
RT "Antiretroviral resistance during successful therapy of HIV type 1  
RT infection";  
RL Proc. Natl. Acad. Sci. U.S.A. 97:10948-10953(2000).  
DR EMBL; AF292799; AAG25407.1; -.  
KW Polypeptide.  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 11 AA; 1386 MW; 79DC73C0145771B4 CRC64;

Query Match 36.0%; Score 18; DB 15; Length 11;  
Best Local Similarity 37.5%; Pred. No. 1e+04;  
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 REPENFK 8  
Db 4 RTPENRLR 11

RESULT 17  
Q9UNV6 PRELIMINARY; PRT; 13 AA.  
AC Q9UNV6;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE Inosine monophosphatase 2 (Fragment).  
GN IMPA2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97463449; PubMed=9322233;  
RA Yoshikawa T., Turner G., Esterling L.E., Sanders A.R.,  
RA Detera-Wadleigh S.D.;  
RT "A novel human myo-inositol monophosphatase gene, IMP.18p, maps to a  
RT susceptibility region for bipolar disorder.";  
RL Mol. Psychiatry 2:393-397(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=10284187;  
RA Yoshikawa T., Padigaru M., Karikera J.D., Sharma M., Berrettini W.H.,  
RA Esterling L.E., Detera-Wadleigh S.D.;  
RT "Genomic structure and novel variants of myo-inositol monophosphatase  
RT 2.";  
RL Mol. Psychiatry 5:165-171(2000).  
DR EMBL; AF085628; AAD22141.1; -.  
DR EMBL; AF085627; AAD22141.1; JOINED.  
FT NON\_TER 1  
FT NON\_TER 13  
SQ SEQUENCE 13 AA; 1491 MW; E8154075786DD401 CRC64;

Query Match 36.0%; Score 18; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFP 3  
Db 7 RFP 9

RESULT 18  
O52840 PRELIMINARY; PRT; 14 AA.  
AC O52840;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
DE Homology with C-terminus of other Rhizobium nodB genes.

OS Rhizobium loti (Mesorhizobium loti).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Phyllobacteriaceae; Mesorhizobium.  
 OX NCBI\_TaxID=381;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97002748; PubMed=8850088;  
 RA Scott D.B., Young C.A., Collins-Emerson J.M., Terzaghi E.A.,  
 RA Rockman E.S., Lewis P.E., Pankhurst C.E.;  
 RT "Novel and complex chromosomal arrangement of Rhizobium loti  
 RT nodulation genes.";  
 RT Mol. Plant Microbe Interact. 9:187-197(1996).  
 RL EMBL: L06241; AAB47352.1; -  
 DR EMBL: L06241; AAB47352.1; -  
 SQ SEQUENCE 14 AA; 1600 MW; 90C26E32C6F34C5 CRC64;

Query Match 36.0%; Score 18; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFP 3  
 Db 9 RFP 11

RESULT 19  
 ID 052636 PRELIMINARY; PRT; 14 AA.  
 AC 052635;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE Tral protein (Fragment).  
 GN TRAL.  
 OS Escherichia coli.  
 OC Plasmid R124.  
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 CC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86059219; PubMed=2999074;  
 RA Frost L.S., Finlay B.B., Oppenorth A., Paranchych W., Lee J.S.;  
 RT "Characterization and sequence analysis of pilin from F-like  
 RT plasmids.";  
 RL J. Bacteriol. 164:1238-1247(1985).  
 DR EMBL: K03092; AAA92759.1; -  
 DR GO: 0046821; C:extrachromosomal DNA; IEA.  
 KW Plasmid.  
 FT NON TER  
 SQ SEQUENCE 14 AA; 1713 MW; 5CCA91188EB30E23 CRC64;

Query Match 36.0%; Score 18; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFP 3  
 Db 12 RFP 14

RESULT 20  
 ID 07X139 PRELIMINARY; PRT; 8 AA.  
 AC 07X139;  
 DT 01-OCT-2003 (TREMBLrel. 25, Created)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE SecE (Fragment).  
 OS Staphylococcus cohnii.  
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
 OX NCBI\_TaxID=29382;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=GIFU9122;  
 RA Morikawa K., Inose Y., Ohta T.;  
 RT "A new Staphylococcal sigma factor in the conserved gene cassette:  
 RT Functional significance and implication for the evolutionary  
 RT processes.";  
 RL Submitted (FEB-2003) to the EMBL/GenBank/DSJ databases.  
 DR EMBL: AY234840; AAO62607.1; -  
 FT NON TER  
 SQ SEQUENCE 8 AA; 1014 MW; F0C9C44B1333D6 CRC64;

Query Match 34.0%; Score 17; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1e+06;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ENF 7  
 Db 5 ENF 7

RESULT 21  
 ID P96421 PRELIMINARY; PRT; 10 AA.  
 AC P96421;  
 DT 01-MAY-1997 (TREMBLrel. 03, Created)  
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)  
 DT 01-NOV-1996 (TREMBLrel. 08, Last annotation update)  
 DE Coded portion of proteolysis tag (Fragment).  
 OS Neisseria gonorrhoeae.  
 CC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
 CC Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=485;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 19424;  
 RX MEDLINE=97128184; PubMed=8972778;  
 RA Williams K.P., Bartel D.P.;  
 RT "Phylogenetic analysis of tmRNA secondary structure.";  
 RL RNA 2:1306-1310(1996).  
 DR EMBL: U68080; AAB48028.1; -  
 FT NON TER  
 SQ SEQUENCE 10 AA; 1038 MW; 857BD22DCB41AB1A CRC64;

Query Match 34.0%; Score 17; DB 2; Length 10;  
 Best Local Similarity 50.0%; Pred. No. 1.4e+04;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 DENFTL 9  
 Db 3 DETVAL 8

RESULT 22  
 ID 09A1Z8 PRELIMINARY; PRT; 11 AA.  
 AC 09A1Z8;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE Tryptophanyl-tRNA synthetase (Fragment).  
 GN TRPS.  
 OS Carsonella ruddii.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Candidatus Carsonella.  
 OX NCBI\_TaxID=114186;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20336438; PubMed=10877784;  
 RA Thao M.L., Moran N.A., Abbot P., Brennan E.B., Burckhardt D.H.,  
 RA Baumann P.;  
 RT "Cospeciation of psyllids and their primary prokaryotic  
 RT endosymbionts.";  
 RL Appl. Environ. Microbiol. 66:2898-2905(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.



RX MEDLINE=21125546; PubMed=11222582;  
 RA Clark M.A.; Baumann L.; Thao M.L.; Moran N.A.; Baumann P.;  
 RT "Regenerative Minimalism in the Genome of a Psyllid Endosymbiont."  
 RL J. Bacteriol. 183:1853-1861(2001).  
 DR EMBL; AF211126; AAK15376.1; -  
 DR GO; GO:0004842; F:RNA ligase activity; IEA.  
 KW Aminoacyl-tRNA synthetase.  
 FT NON\_TER 1  
 SQ SEQUENCE 11 AA; 1384 MW; 07A038324339C724 CRC64;

Query Match 34.0%; Score 17; DB 2; Length 11;  
 Best Local Similarity 60.0%; Pred. No. 1.6e+04;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 ENFKL 9  
 DB 7 KNFNL 11

## RESULT 23

Q9TWV4 PRELIMINARY; PRT; 12 AA.  
 AC Q9TWV4;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE Light yellow cell peptide (Fragment).  
 OS Lymnaea stagnalis (Great pond snail).  
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;  
 CC Lymnaeidae; Lymnaeidae; Lymnaea.  
 NCBI\_TaxID=6523;  
 RX MEDLINE=93095719; PubMed=1334202;  
 RA Hoek R.M.; Li K.W.; van Minnen J.; Geraerts W.P.;  
 RT "Chemical characterization of a novel peptide from the neuroendocrine  
 RL light yellow cells of Lymnaea stagnalis."  
 RL Brain Res. Mol. Brain Res. 16:71-74(1992).  
 DR PIR; A56878; A56878.  
 FT NON\_TER 1  
 FT NON\_TER 12  
 SQ SEQUENCE 12 AA; 1385 MW; 44255417732045B3 CRC64;

Query Match 34.0%; Score 17; DB 5; Length 12;  
 Best Local Similarity 42.9%; Pred. No. 1.7e+04;  
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 PDENFKL 9  
 DB 3 PDKSTLL 9

## RESULT 24

Q9RSR5 PRELIMINARY; PRT; 14 AA.  
 AC Q9RSR5;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE 25-kDa elastin-binding protein (Fragment).  
 OS Staphylococcus aureus.  
 CC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
 NCBI\_TaxID=1280;  
 RX MEDLINE=92078218; PubMed=1744133;  
 RA Park P.W.; Roberts D.D.; Grosso L.E.; Parks W.C.; Rosenblom J.;  
 RT "Binding of elastin to Staphylococcus aureus."  
 RL J. Biol. Chem. 266:23399-23406(1991).  
 DR PIR; A41589; A41589.  
 FT NON\_TER 1  
 FT NON\_TER 14

SQ SEQUENCE 14 AA; 1754 MW; 96CA3586E99D1CCA CRC64;

Query Match 34.0%; Score 17; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 2e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NFK 8  
 DB 3 NFK 5

## RESULT 25

P78359 PRELIMINARY; PRT; 14 AA.  
 ID P78359;  
 AC P78359;  
 DT 01-MAY-1997 (TREMBLrel. 03, Created)  
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE NF-kappa-B transcription factor p65 (Fragment).  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NCBI\_TaxID=9606;  
 RX MEDLINE=93095719; PubMed=1334202;  
 RA Hoek R.M.; Li K.W.; van Minnen J.; Geraerts W.P.;  
 RT "Chemical characterization of a novel peptide from the neuroendocrine  
 RL light yellow cells of Lymnaea stagnalis."  
 RL Brain Res. Mol. Brain Res. 16:71-74(1992).  
 DR PIR; A56878; A56878.  
 FT NON\_TER 1  
 FT NON\_TER 12  
 SQ SEQUENCE 12 AA; 1385 MW; 44255417732045B3 CRC64;

Query Match 34.0%; Score 17; DB 4; Length 14;  
 Best Local Similarity 66.7%; Pred. No. 2e+04;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 DENFKL 9  
 DB 2 DELFPL 7

## RESULT 26

Q9JUT5 PRELIMINARY; PRT; 14 AA.  
 ID Q9JUT5;  
 AC Q9JUT5;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE B-Raf protein (Fragment).  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RX MEDLINE=92078218; PubMed=1744133;  
 RA Barnier J.V.; Papin C.; Eychene A.; Iecog O.;  
 RT "The mouse B-raf gene encodes multiple protein isoforms with tissue-  
 specific expression."  
 RL U. Biochem. 270:23381-23389(1995).  
 DR EMBL; AJ276308; CAB81556.1; -  
 FT NON\_TER 1  
 FT NON\_TER 14  
 SQ SEQUENCE 14 AA; 1748 MW; D1E0505C44927F02 CRC64;

Query Match 34.0%; Score 17; DB 11; Length 14;  
 Best Local Similarity 75.0%; Pred. No. 2e+04;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 DENF 7  
Db 1 DEKF 4

## RESULT 27

093LE4 PRELIMINARY; PRT; 9 AA.  
AC 093LE4; 01-DEC-2001 (TRENBLREL. 19, Created)  
DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)  
DE 01-DEC-2001 (TRENBLREL. 19, Last annotation update)  
OS Proteolysis tag (Fragment).  
OC Helicobacillus mobilis.  
OS Bacteria; Firmicutes; Clostridia; Clostridiales; Helicobacteriaceae;  
OC Helicobacillus.  
OX NCBI\_TaxID=28064;  
RN SEQUENCE FROM N.A.  
RX MEDLINE=20063247; PubMed=10592213;  
RA Williams K.P.;  
RT "The tRNA website";  
RL Nucleic Acids Res. 28:168-168(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Williams K.P.;  
RT "Phylogenetic analysis of tRNA";  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY040838; AAK83526.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 9 AA; 937 MW; 7CD8D72DCB544AAB CRC64;

Query Match 32.0%; Score 16; DB 2; Length 9;  
Best Local Similarity 33.3%; Pred. No. 1e+06;  
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 DENF 9  
Db 2 EDNYAL 7

## RESULT 28

047604 PRELIMINARY; PRT; 11 AA.  
AC 047604; 01-NOV-1996 (TRENBLREL. 01, Created)  
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)  
DE 01-DEC-2001 (TRENBLREL. 19, Last annotation update)  
OS REase protein (Fragment).  
DE REase.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9139577; PubMed=1995588;  
RA Tao T.; Bourne J.C.; Blumenthal R.M.;  
RT "A family of regulatory genes associated with type II restriction-modification systems";  
RL J. Bacteriol. 173:1367-1375(1991).  
DR EMBL; M63621; AAA24560.1; -.  
FT NON\_TER 11  
SQ SEQUENCE 11 AA; 1296 MW; 3039A71A34472AB7 CRC64;

Query Match 32.0%; Score 16; DB 2; Length 11;  
Best Local Similarity 75.0%; Pred. No. 2.4e+04;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PDEN 6

Db 4 PDLN 7

## RESULT 29

Q81VH0 PRELIMINARY; PRT; 12 AA.  
AC Q81VH0; 01-MAR-2003 (TRENBLREL. 23, Created)  
DT 01-MAR-2003 (TRENBLREL. 23, Last sequence update)  
DE 01-MAR-2003 (TRENBLREL. 23, Last annotation update)  
OS Truncated PAX6 protein (Fragment).  
GN PAX6.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Neethirajan G.; Krishnas S.R.; Vijayalakshmi P.; Sundaresan P.;  
RT "Mutation analysis in Human PAX6 gene of Aniridia";  
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF548390; AAN66817.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 12 AA; 1511 MW; 9E169541A67B51F1 CRC64;

Query Match 32.0%; Score 16; DB 4; Length 12;  
Best Local Similarity 66.7%; Pred. No. 2.7e+04;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FPD 4  
Db 7 YPD 9

## RESULT 30

Q88577 PRELIMINARY; PRT; 12 AA.  
AC Q88577; 01-NOV-1996 (TRENBLREL. 01, Created)  
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)  
DE 01-DEC-2001 (TRENBLREL. 19, Last annotation update)  
OS Theiler's murine encephalomyelitis virus 5' flank and 5' end cds (Fragment).  
OS Theiler's encephalomyelitis virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;  
OC Cardiovirus.  
OX NCBI\_TaxID=12124;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=TO(4);  
RA MEDLINE=92194426; PubMed=1549749;  
RA Pritchard A.B.; Calenoff M.A.; Simpson S.; Jensen K.; Lipson H.L.;  
RT "A single base deletion in the 5' noncoding region of Theiler's virus attenuates neurovirulence";  
RL J. Virol. 66:1951-1958(1992).  
DR EMBL; M80885; AAN73156.1; -.  
FT NON\_TER 12  
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match 32.0%; Score 16; DB 12; Length 12;  
Best Local Similarity 66.7%; Pred. No. 2.7e+04;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FPD 4  
Db 7 YPD 9

## RESULT 31

Q88578 PRELIMINARY; PRT; 12 AA.  
AC Q88578; 01-NOV-1996 (TRENBLREL. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds  
DE (Fragment).  
OS Theiler's encephalomyelitis virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;  
OC Cardiovirus.  
OX NCBI\_TaxID=12124;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=TO(B15);  
RX MEDLINE=92194426; PubMed=1548749;  
RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;  
RT "A single base deletion in the 5' noncoding region of Theiler's virus  
attenuates neurovirulence."  
RL J. Virol. 66:1951-1958(1992).  
DR EMBL; M80886; AAA73157.1; -.  
FT NON\_TER 12 12  
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match. 32.0%; Score 16; DB 12; Length 12;  
Best Local Similarity 66.7%; Pred. No. 2.7e+04;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FPD 4  
DB 7 YPD 9

## RESULT 32

ID 088579 PRELIMINARY; PRT; 12 AA.  
AC 088579;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds  
DE (Fragment).  
OS Theiler's encephalomyelitis virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;  
OC Cardiovirus.  
OX NCBI\_TaxID=12124;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=VL;  
RX MEDLINE=92194426; PubMed=1548749;  
RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;  
RT "A single base deletion in the 5' noncoding region of Theiler's virus  
attenuates neurovirulence."  
RL J. Virol. 66:1951-1958(1992).  
DR EMBL; M80887; AAA73158.1; -.  
FT NON\_TER 12 12  
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match. 32.0%; Score 16; DB 12; Length 12;  
Best Local Similarity 66.7%; Pred. No. 2.7e+04;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FPD 4  
DB 7 YPD 9

## RESULT 33

ID 088575 PRELIMINARY; PRT; 12 AA.  
AC 088575;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds  
DE (Fragment).  
OS Theiler's encephalomyelitis virus.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;  
OC Cardiovirus.  
OX NCBI\_TaxID=12124;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PA;  
RX MEDLINE=92194426; PubMed=1548749;  
RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;  
RT "A single base deletion in the 5' noncoding region of Theiler's virus  
attenuates neurovirulence."  
RL J. Virol. 66:1951-1958(1992).  
DR EMBL; M80883; AAA73154.1; -.  
FT NON\_TER 12 12  
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match. 32.0%; Score 16; DB 12; Length 12;  
Best Local Similarity 66.7%; Pred. No. 2.7e+04;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FPD 4  
DB 7 YPD 9

## RESULT 34

ID 088580 PRELIMINARY; PRT; 12 AA.  
AC 088580;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds  
DE (Fragment).  
OS Theiler's encephalomyelitis virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;  
OC Cardiovirus.  
OX NCBI\_TaxID=12124;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=VALYUSK;  
RX MEDLINE=92194426; PubMed=1548749;  
RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;  
RT "A single base deletion in the 5' noncoding region of Theiler's virus  
attenuates neurovirulence."  
RL J. Virol. 66:1951-1958(1992).  
DR EMBL; M80888; AAA73159.1; -.  
FT NON\_TER 12 12  
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match. 32.0%; Score 16; DB 12; Length 12;  
Best Local Similarity 66.7%; Pred. No. 2.7e+04;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FPD 4  
DB 7 YPD 9

## RESULT 35

ID 088582 PRELIMINARY; PRT; 12 AA.  
AC 088582;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds  
DE (Fragment).  
OS Theiler's encephalomyelitis virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;  
OC Cardiovirus.  
OX NCBI\_TaxID=12124;  
RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN=TO(Yale);  
 RX MEDLINE=92194426; PubMed=1548749;  
 RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;  
 RT "A single base deletion in the 5' noncoding region of Theiler's virus  
 attenuates neurovirulence.";  
 RL J. Virol. 66:1951-1958(1992).  
 DR EMBL; M80890; AAA73151.1; -.  
 FT NON TER  
 SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match 32.0%; Score 16; DB 12; Length 12;  
 Best Local Similarity 66.7%; Pred. No. 2.7e+04;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FPD 4  
 DB 7 YPD 9

RESULT 36  
 ID Q8581 PRELIMINARY; PRT; 12 AA.  
 AC Q8581;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds  
 DE (Fragment).  
 OS Theiler's encephalomyelitis virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;  
 OC Cardiovirus.  
 OX NCBI\_TaxID=12124;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MW;  
 RX MEDLINE=92194426; PubMed=1548749;  
 RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;  
 RT "A single base deletion in the 5' noncoding region of Theiler's virus  
 attenuates neurovirulence.";  
 RL J. Virol. 66:1951-1958(1992).  
 DR EMBL; M80889; AAA73150.1; -.  
 FT NON TER  
 SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match 32.0%; Score 16; DB 12; Length 12;  
 Best Local Similarity 66.7%; Pred. No. 2.7e+04;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FPD 4  
 DB 7 YPD 9

RESULT 37  
 ID Q8576 PRELIMINARY; PRT; 12 AA.  
 AC Q8576;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds  
 DE (Fragment).  
 OS Theiler's encephalomyelitis virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;  
 OC Cardiovirus.  
 OX NCBI\_TaxID=12124;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MW;  
 RX MEDLINE=92194426; PubMed=1548749;  
 RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;  
 RT "A single base deletion in the 5' noncoding region of Theiler's virus  
 attenuates neurovirulence.";

RL J. Virol. 66:1951-1958(1992).  
 DR EMBL; M80884; AAA73155.1; -.  
 FT NON TER  
 SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match 32.0%; Score 16; DB 12; Length 12;  
 Best Local Similarity 66.7%; Pred. No. 2.7e+04;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FPD 4  
 DB 7 YPD 9

RESULT 38  
 ID Q865C9 PRELIMINARY; PRT; 13 AA.  
 AC Q865C9;  
 DT 01-JUN-2003 (TREMBLrel. 24, Created)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE Glutamine synthetase (Fragment).  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kim U.G., Vallet J.L., Christenson R.K.;  
 RT "Characterization of porcine glutamine synthetase.";  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY216477; AAO64254.1; -.  
 FT NON TER  
 SQ SEQUENCE 13 AA; 1555 MW; 87987A0B71AB6B1A CRC64;

Query Match 32.0%; Score 16; DB 6; Length 13;  
 Best Local Similarity 60.0%; Pred. No. 2.9e+04;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 DENPK 8  
 DB 6 DEFPQ 10

RESULT 39  
 ID Q8SL68 PRELIMINARY; PRT; 13 AA.  
 AC Q8SL68;  
 DT 01-JUN-2002 (TREMBLrel. 21, Created)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE Psba (Fragment).  
 GN PSBA.  
 OS Monanthus anagensis.  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Saxifragales; Crassulaceae; Monanthus.  
 OX NCBI\_TaxID=91110;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Mort M.E., Soltis D.E., Soltis P.S., Francisco J., Santos A.;  
 RT "Evolution and diversification of the Macaronesian clade of  
 Crassulaceae.";  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY082189; AAM13933.1; -.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON TER  
 SQ SEQUENCE 13 AA; 1361 MW; C0FB1BDAD15CB02 CRC64;

Query Match 32.0%; Score 16; DB 8; Length 13;  
 Best Local Similarity 60.0%; Pred. No. 2.9e+04;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PPDEN 6  
Db 8 FPSIN 12

## RESULT 40

Q83171 PRELIMINARY; PRT; 13 AA.  
AC Q83171;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Hypothetical protein (Fragment).  
OS Cauliflower mosaic virus.  
OC Viruses; Retroid viruses; Caulimoviridae; Caulimovirus.  
OC NCBI\_TaxID=10641;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=8155790; PubMed=2894473;  
RA Penswick J., Hubler R., Kohn T.;  
RT "A viable mutation in cauliflower mosaic virus, a retroviruslike plant virus, separates its capsid protein and polymerase genes."  
RL J. Virol. 62:1460-1463(1988).  
DR EMBL; M19741; AAA6605.1; -.  
KW Hypothetical protein.  
FT NON TER 1  
SQ SEQUENCE 13 AA; 1600 MW; 5DD9E7FDC45CB13 CRC64;

Query Match 32.0%; Score 16; DB 12; Length 13;  
Best Local Similarity 50.0%; Pred. No. 2.9e+04;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 PDENFK 8  
Db 4 PKEFK 9

## RESULT 41

O8UJ32 PRELIMINARY; PRT; 13 AA.  
AC O8UJ32;  
DT 01-OCT-2002 (TREMBlrel. 22, Created)  
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
DE 37LRP/p40 (Fragment).  
OS Ficedula albicollis.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Passeriformes; Muscicapidae; Ficedula.  
OC NCBI\_TaxID=59894;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=B8;  
RA MEDLINE=21918460; PubMed=11918793;  
RA Primer C.R., Boyce T., Lindell J., Saetre G.-P.;  
RT "Single-nucleotide polymorphism characterization in species with RT limited available sequence information: high nucleotide diversity revealed in the avian genome."  
RL Mol. Ecol. 11:603-612(2002).  
DR EMBL; AF454232; AAM22911.1; -.  
FT NON TER 1  
SQ SEQUENCE 13 AA; 1674 MW; 18331625CF9559DB CRC64;

Query Match 32.0%; Score 16; DB 13; Length 13;  
Best Local Similarity 60.0%; Pred. No. 2.9e+04;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPPDE 5  
Db 9 RDPDE 13

## RESULT 42

O55326 PRELIMINARY; PRT; 14 AA.  
AC O55326;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE Putative ORF1 (Fragment).  
OS Synecococcus sp. (strain PCC 7002) (Agmenellum quadruplicatum).  
OC Bacteria; Cyanobacteria; Chroococcales; Synecococcus.  
OC NCBI\_TaxID=32049;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=PR6;  
RX MEDLINE=92201692; PubMed=1551590;  
RA Rhee E., Skirwale V.L., Gasparich G.E., Bryant D.A.;  
RT "The psac genes of Synecococcus sp. PCC7002 and Cyanophora paradoxa: cloning and sequence analysis."  
RL Gene 112:123-128(1992).  
DR EMBL; M66238; AAA27351.1; -.  
FT NON TER 14  
SQ SEQUENCE 14 AA; 1590 MW; 9D5226BDCB9398BCA CRC64;

Query Match 32.0%; Score 16; DB 2; Length 14;  
Best Local Similarity 60.0%; Pred. No. 3.1e+04;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 ENFKL 9  
Db 2 KGFKL 6

## RESULT 43

O8V3U6 PRELIMINARY; PRT; 14 AA.  
AC O8V3U6;  
DT 01-MAR-2002 (TREMBlrel. 20, Created)  
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
DE Tomato yellow leaf curl virus TYLCV/TYLCV recombinant isolate Spain ES42199 CI (Fragment).  
OS Tomato yellow leaf curl virus (TYLCV).  
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.  
OC NCBI\_TaxID=10832;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=TYLCV/TYLCV recombinant isolate Spain ES42199;  
RA Monci F., Navas-Castillo J., Moriones E.;  
RT "Evidence of the occurrence of a natural recombinant between Tomato yellow leaf curl virus."  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF401478; AAL59158.1; -.  
FT NON TER 14  
SQ SEQUENCE 14 AA; 1710 MW; D296A16BF41A7FD9 CRC64;

Query Match 32.0%; Score 16; DB 13; Length 14;  
Best Local Similarity 28.6%; Pred. No. 3.1e+04;  
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 PDENFKL 9  
Db 3 PPKRFQI 9

## RESULT 44

P72279 PRELIMINARY; PRT; 8 AA.  
AC P72279;  
DT 01-FEB-1997 (TREMBlrel. 02, Created)  
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE Biphenyl dioxygenase (Fragment).

GN BPHB.  
 OS Rhodococcus globerulus.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacteriaceae; Nocardiaceae; Rhodococcus.  
 OK NCBI\_TaxID=33008;  
 RN  
 RP  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95255652; PubMed=7737502;  
 RA Asturias J.A., Diaz E., Timmis K.N.;  
 RT "Evolutionary relationship of the biphenyl dioxygenase of the gram-  
 positive bacterium Rhodococcus globerulus p6 to multicomponent  
 dioxygenases of gram-negative bacteria.";  
 RL Gene 156:11-18(1995).  
 DR EMBL; X80041; CAA56350.1;  
 DR GO; GO:0016702; F:oxidoreductase activity, acting on single d. . . ; IEA.  
 KM Dioxygenase.  
 FT NON TER  
 SQ SEQUENCE 8 AA; 989 MW; EBD2CB1AB6D73406 CRC64;

Query Match 30.0%; Score 15; DB 2; Length 8;  
 Best Local Similarity 60.0%; Pred. No. 1e+06;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 RFPDE 5  
 1 1 1 1 1 1  
 DB 2 RLQDE 6

## RESULT 45

07T282 PRELIMINARY; PRT; 8 AA.  
 ID 07T282  
 AC 07T282;  
 DT 01-OCT-2003 (TREMBlrel. 25. Created)  
 DT 01-OCT-2003 (TREMBlrel. 25; last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25; last annotation update)  
 DE Calmodulin (Fragment).  
 OS Geophilone nigra (Galapagos giant tortoise).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Testudines; Cryptodira; Testudinoidea; Testudinidae; Geochelone.  
 OK NCBI\_TaxID=66189;  
 RN  
 RP  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ESP1;  
 RA Gentile G., Burns C., Sezi E., Bergman W., Powell J.R., Caccione A.;  
 RT "Contrasting Patterns of Nuclear and Mitochondrial DNA Variation in  
 the Giant Galapagos Tortoise.";  
 RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY101722; AAW47127.1; -.  
 FT NON TER  
 FT NON TER  
 SQ SEQUENCE 8 AA; 892 MW; 5D0769CAA041A874 CRC64;

Query Match 30.0%; Score 15; DB 13; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 1e+06;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 FPD 4  
 1 1 1 1 1 1  
 DB 6 FPE 8

Search completed: August 30, 2004, 10:55:26  
 Job time : 10.6655 secs



DT 28-FEB-2003 (Rel. 41, last annotation update)  
 DE Neb-FIRamide 1.  
 OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 CC Sarcophagidae; Sarcophaga.  
 OK NCBI\_TaxId=7385;  
 RN [1]  
 RP SEQUENCE, AMIDATION, AND FUNCTION.  
 RC TISSUE=CNS;  
 RX MEDLINE=22342733; PubMed=12438685;  
 RA Meusen T., Mertens I., Clynen E., Baggerman G., Nichols R.,  
 RA Nachman R.J., Huybrechts R., De Loof A., Schoofs L.;  
 RT "Identification in *Drosophila melanogaster* of the invertebrate G  
 RT protein-coupled FMRFamide receptor.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368 (2002).  
 CC -! FUNCTION: Has modulatory actions at skeletal neuromuscular  
 CC junctions.  
 CC -! SUBCELLULAR LOCATION: Secreted.  
 CC -! SIMILARITY: Belongs to the FARP (FMRFamide related peptide)  
 CC family.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 12 12  
 SQ SEQUENCE 12 AA; 1389 MW; 2DC45519C14B5A7 CRC64;

Query Match 42.0%; Score 21; DB 1; Length 12;  
 Best Local Similarity 60.0%; Pred. No. 3.1e+02;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 PDENF 7  
 DB 5 PSDNF 9

RESULT 3  
 EFG\_CLOPA STANDARD; PRT; 11 AA.  
 AC P81350;  
 DT 15-JUL-1998 (Rel. 35, Created)  
 DT 15-JUL-1998 (Rel. 35, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Elongation factor G (EF-G) (CP 5) (Fragment).  
 GN FUSA.  
 OS Clostridium pasteurianum.  
 CC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 CC Clostridium.  
 OK NCBI\_TaxId=1501;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=M5;  
 RX MEDLINE=98291870; PubMed=9629918;  
 RA Flensburg R., Skjeldal L.;  
 RT "Two-dimensional gel electrophoresis separation and N-terminal  
 RT sequence analysis of proteins from *Clostridium pasteurianum* M5.";  
 RL Electrophoresis 19:802-806 (1998).  
 CC -! FUNCTION: This protein promotes the GTP-dependent translocation of  
 CC the nascent protein chain from the A-site to the P-site of the  
 CC ribosome.  
 CC -! SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -! SIMILARITY: Belongs to the GTP-binding elongation factor family.  
 CC EF-G/EF-2 subfamily.  
 DR InterPro; IPR000795; EF\_GTPbind.  
 DR PROSITE; PS00301; EFACFOTR\_GTP; PARTIAL.  
 KW Elongation factor; Protein biosynthesis; GTP-binding.  
 FT NON TER 11  
 SQ SEQUENCE 11 AA; 1337 MW; 412E71F1D9C3B17 CRC64;

Query Match 40.0%; Score 20; DB 1; Length 11;  
 Best Local Similarity 37.5%; Pred. No. 4.3e+02;  
 Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 RFPDENF 8  
 DB 1 RFPDENF 8

DB 1 KYPLEKFG 8

RESULT 4  
 LPER\_BACLI STANDARD; PRT; 14 AA.  
 ID LPER\_BACLI  
 AC Q04303;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Erythromycin resistance leader peptide (23S rRNA methylase leader  
 DE peptide).  
 OS Bacillus licheniformis, and  
 OS Bacillus anthracis.  
 CC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OK NCBI\_TaxId=1402, 1392;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=B.licheniformis;  
 RX MEDLINE=84245158; PubMed=6429477;  
 RA Gryczan T., Israeli-Reches M., del Bue M., Dubnau D.;  
 RT "DNA sequence and regulation of ermD, a macrolide-lincosamide-  
 RT streptogramin B resistance element from *Bacillus licheniformis*.";  
 RL Mol. Gen. Genet. 194:349-356 (1984).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=B.licheniformis; STRAIN=EMR-1;  
 RX MEDLINE=91310580; PubMed=1713206;  
 RA Kwak J.-K., Choi E.-C., Weisblum B.;  
 RT "Transcriptional attenuation control of ermK, a  
 RT macrolide-lincosamide-streptogramin B resistance determinant from  
 RT *Bacillus licheniformis*.";  
 RL J. Bacteriol. 173:4725-4735 (1991).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=B.anthracis; STRAIN=590;  
 RX MEDLINE=93232776; PubMed=8473865;  
 RA Kim H.-S., Choi E.-C., Kim B.-K.;  
 RT "A macrolide-lincosamide-streptogramin B resistance determinant from  
 RT *Bacillus anthracis* 590: cloning and expression of ermD.";  
 RL J. Gen. Microbiol. 139:601-607 (1993).  
 CC -! FUNCTION: THIS PEPTIDE IS INVOLVED IN THE CONTROL MECHANISM OF  
 CC THE SYNTHESIS OF THE MACROLIDE-LINCOSAMIDE-STREPTOGRAMIN B  
 CC RESISTANCE PROTEIN. IT ACTS AS A TRANSCRIPTIONAL ATTENUATOR.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC  
 DR EMBL; L08389; AAA22586.1; -  
 DR EMBL; M29832; AAA22598.1; -  
 DR PIR; A42473; A42473.  
 KW Antibiotic resistance; Leader peptide.  
 SQ SEQUENCE 14 AA; 1732 MW; 5D138B59F2ED07 CRC64;

Query Match 40.0%; Score 20; DB 1; Length 14;  
 Best Local Similarity 66.7%; Pred. No. 5.6e+02;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 RFPDEN 6  
 DB 8 RFPDEN 13

RESULT 5  
 FAR2\_MACRS STANDARD; PRT; 8 AA.  
 ID FAR2\_MACRS  
 AC P83375;  
 DT 28-FEB-2003 (Rel. 41, Created)



DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE FMRamide-like neuropeptide FLP2 (ADKNFLRF-amide).  
 OS Macrobrachium rosenbergii (Giant Fresh water prawn).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;  
 CC Palaemonidae; Palaemonidae; Macrobrachium.  
 NCBI\_TaxID=79674;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Eyestalk;  
 RA Sitihingnui P., Sarathongkum W., Jaidechoey S., Longyant S.,  
 RT "Novel FMRamide-like neuropeptides from the eyestalk of the giant  
 RT freshwater prawn Macrobrachium rosenbergii.";  
 RL Comp. Biochem. Physiol. 130B:587-595(1998).  
 CC -1- MASS SPECTROMETRY: MW=1009.4; METHOD=MALDI.  
 CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)  
 CC family.  
 DR GO:0007218; P:neuropeptide signaling pathway; TMS.  
 KM Neuropeptide; Amidation.  
 FT MOD RES 8  
 SQ SEQUENCE 8 AA; 1010 MW; 9CD40729C4433AAD CRC64;  
 Query Match 38.0%; Score 19; DB 1; Length 8;  
 Best Local Similarity 75.0%; Pred. No. 1.4e+05;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DENF 7  
 DB 2 DKNF 5

RESULT 6  
 ID FARP3\_MACRS STANDARD; PRT; 9 AA.  
 AC P83276;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE FMRamide-like neuropeptide FLP3 (NYDKNFLRF-amide).  
 OS Macrobrachium rosenbergii (Giant Fresh water prawn).  
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;  
 CC Palaemonidae; Palaemonidae; Macrobrachium.  
 NCBI\_TaxID=79674;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Eyestalk;  
 RA Sitihingnui P., Sarathongkum W., Jaidechoey S., Longyant S.,  
 RT "Novel FMRamide-like neuropeptides from the eyestalk of the giant  
 RT freshwater prawn Macrobrachium rosenbergii.";  
 RL Comp. Biochem. Physiol. 120B:587-595(1998).  
 CC -1- MASS SPECTROMETRY: MW=1215.4; METHOD=MALDI.  
 CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)  
 CC family.  
 DR GO:0007218; P:neuropeptide signaling pathway; TMS.  
 KM Neuropeptide; Amidation.  
 FT MOD RES 9  
 SQ SEQUENCE 9 AA; 1216 MW; 18220729C4433ABB CRC64;  
 Query Match 38.0%; Score 19; DB 1; Length 9;  
 Best Local Similarity 75.0%; Pred. No. 1.4e+05;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DENF 7  
 DB 3 DKNF 6

RESULT 7  
 FARP7\_MACRS

ID FARP7\_MACRS STANDARD; PRT; 10 AA.  
 AC P83280;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE FMRamide-like neuropeptide FLP7 (GYDKNFLRF-amide).  
 OS Macrobrachium rosenbergii (Giant Fresh water prawn).  
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;  
 CC Palaemonidae; Palaemonidae; Macrobrachium.  
 NCBI\_TaxID=79674;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Eyestalk;  
 RA Sitihingnui P., Sarathongkum W., Longyant S., Panchan N.,  
 RT MEDLINE=21107394; Pubmed=11179812;  
 RA Sitihingnui P., Sarathongkum W., Longyant S., Panchan N.,  
 RA Sitihingnui W., Petsom A.;  
 RT "Three more novel FMRamide-like neuropeptide sequences from the  
 RT eyestalk of the giant freshwater prawn Macrobrachium rosenbergii.";  
 RL Peptides 22:191-197(2001).  
 CC -1- MASS SPECTROMETRY: MW=1244.9; METHOD=MALDI.  
 CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)  
 CC family.  
 DR GO:0007218; P:neuropeptide signaling pathway; IDA.  
 KM Neuropeptide; Amidation.  
 FT MOD RES 10  
 SQ SEQUENCE 10 AA; 1244 MW; 3CFB9C29C4540AA8 CRC64;  
 Query Match 38.0%; Score 19; DB 1; Length 10;  
 Best Local Similarity 50.0%; Pred. No. 6.1e+02;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDNF 7  
 DB 2 YGDKNF 7

RESULT 8  
 ID SLAP\_BACTG STANDARD; PRT; 10 AA.  
 AC P49325;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE S-layer protein (surface layer protein) (Fragment).  
 OS Bacillus thuringiensis (subsp. galleriae).  
 CC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 NCBI\_TaxID=29338;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=NRRL 4045;  
 RX MEDLINE=90078111; Pubmed=2592346;  
 RA Luckey M.D., Beveridge T.J.;  
 RT "Characterization of a dynamic S layer on Bacillus thuringiensis.";  
 RL J. Bacteriol. 171:6656-6667(1989).  
 CC -1- FUNCTION: The S-layer is a paracrystalline mono-layered assembly  
 CC of proteins which coat the surface of bacteria.  
 CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A  
 CC S-LAYER WITH OBLIQUE (P2) SYMMETRY.  
 DR PIR; A60476; A60476.  
 KM Cell wall; S-layer.  
 FT NON TER 10  
 SQ SEQUENCE 10 AA; 1080 MW; 57AECACAB769D1A3 CRC64;  
 Query Match 38.0%; Score 19; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FPD 4  
 DB 5 FPD 7

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RESULT 9
ALILI_CYPDPO STANDARD; PRT; 8 AA.
ID ALILI_CYPDPO
AC P82152;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydia pomonella (Codling moth).
OC Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_Taxid=82600;
RN [1]
RP SEQUENCE.
RC TISSUE=Larva;
RA MEDLINE=36054539; PubMed=9392829;
RA Duvé H., Johnson A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309(1997).
CC -1- SIMILARITY: Belongs to the allatostatin family.
KM Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 934 MW; C82879C45B51F775 CRC64;

Query Match 36.0%; Score 18; DB 1; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.4e+05;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CY 3 DENF 9
DB 2 PHYNFGL 8

RESULT 10
FARL_PENMO STANDARD; PRT; 8 AA.
ID FARL_PENMO
AC P83316;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRFamide-like neuropeptide FLPL (GPRNPLRF-amide).
OC Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_Taxid=66867;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RA MEDLINE=21956277; PubMed=11959015;
RA Stichgornigul P., Pupum U., Krungkasem C., Longyant S.,
RA Chaitisutangkura P., Stichgornigul W., Petsom A.;
RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Penaeus monodon.";
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=1024.8; METHOD=MALDI.
CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
family.
DR GO:0007218; P:neuropeptide signaling pathway; TMS.
KM Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 1024 MW; 72D40729C4540A8 CRC64;

Query Match 36.0%; Score 18; DB 1; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 4 DENF 7
DB 2 DRNF 5

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RESULT 11
FAR3_HOMAM STANDARD; PRT; 8 AA.
ID FAR3_HOMAM
AC P41486;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFamide-like neuropeptide 3 (FLI 3) (F2).
OC Homarus americanus (American lobster).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Nebroipoidea; Nephropidae; Homarus.
OX NCBI_Taxid=6706;
RN [1]
RP SEQUENCE.
RC TISSUE=Pericardial organs;
RA MEDLINE=88116164; PubMed=3429714;
RA Trimmer B.A., Koblerki L.A., Kravitz B.A.;
RT "Purification and characterization of FMRFamide-like immunoreactive
RT substances from the lobster nervous system: Isolation and sequence
RT analysis of two closely related peptides.";
RL J. Comp. Neurol. 266:16-26(1987).
CC -1- MISCELLANEOUS: Pericardial organs release this peptide with 100 mM
potassium in the presence of calcium.
CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
family.
KM Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 1054 MW; C6D40729C4540A8 CRC64;

Query Match 36.0%; Score 18; DB 1; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 4 DENF 7
DB 2 DRNF 5

RESULT 12
UC26_MAIZE STANDARD; PRT; 8 AA.
ID UC26_MAIZE
AC P80632;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 907)
(Fragment).
OC Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoidae; Andropogoneae; Zea.
OX NCBI_Taxid=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Toullet P., Ricciardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
protein is: 7.0, its MW is: 57.2 kDa.
DR Maize-2DPAGE; P80632; COLEOPTILE.
KM Maize-2DPAGE; P80632; COLEOPTILE.
FT NON_TER 1
FT TER 8
SQ SEQUENCE 8 AA; 990 MW; 9639D6DA8176BD CRC64;

Query Match 36.0%; Score 18; DB 1; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

QY 3 PDENFX 8  
| : |  
3 PRDQFX 8

## RESULT 13

UPA3 HUMAN STANDARD; PRT; 9 AA.  
AC P30069;  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Unknown protein from 2D-page of plasma (Spot 11) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Plasma;  
RX MEDLINE=93092937; PubMed=1459097;  
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,  
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,  
RA Hochstrasser D.F.,  
RT "Plasma protein map: an update by microsequencing."  
RL Electrophoresis 13:707-714(1992).  
CC -I- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
CC protein is: 4.6, its MW is: 46 kDa.  
DR SWISS-2DPAGE: P30069; HUMAN.  
FT NON\_TER  
FT SEQUENCE 9 AA; 1056 MW; 26F2B1BAF769C737 CRC64;  
SQ

Query Match 36.0%; Score 18; DB 1; Length 9;  
Best Local Similarity 50.0%; Pred. No. 1.4e+05;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PDENF 7  
| : |  
4 PPXTDF 9

## RESULT 14

TKN1\_PSEGU STANDARD; PRT; 11 AA.  
AC P42986;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Kasinin-like peptide K-1 (PG-KI).  
OS Pseudophryne guentheri (Guenther's toadlet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
OC Myobatrachinae; Pseudophryne.  
OX NCBI\_TaxID=30349;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=90287814; PubMed=2356157;  
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
RA Roberts J.D., Melchiorri P., Espamer V.,  
RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
RT the Australian frog Pseudophryne guentheri.",  
RT Peptides 11:299-304(1990).  
CC -I- FUNCTION: Tachykynins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretegogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC -I- SUBCELLULAR LOCATION: Secreted.  
CC -I- TISSUE SPECIFICITY: Skin.  
CC -I- SIMILARITY: Belongs to the tachykinin family.  
DR PIR, B60409; B60409.

DR InterPro; IPR002040; Tachy\_Neurokinin.  
DR InterPro; IPR008215; Tachykinin.  
DR Pfam; PF02202; Tachykinin; 1.  
DR SMART; SM00203; TK; 1.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
KW Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1  
FT MOD\_RES 11 11  
FT SEQUENCE 11 AA; 1269 MW; 3DBA7C37C9CB1A57 CRC64;  
SQ

Query Match 36.0%; Score 18; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDE 5  
| : |  
4 PDE 6

## RESULT 15

TKN1\_UPERU STANDARD; PRT; 11 AA.  
AC P08612;  
DT 01-AUG-1988 (Rel. 08, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Uperolein.  
OS Uperoleia rugosa (Wrinkled toadlet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
OC Myobatrachinae; Uperoleia.  
OX NCBI\_TaxID=8368;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=75131227; PubMed=1120493;  
RA Anastasi A., Espamer V., Endean R.,  
RT "Structure of uperolein, a physalaemin-like endecapeptide occurring  
RT in the skin of Uperoleia rugosa and Uperoleia marmorata.",  
RL Experientia 31:394-395(1975).  
CC -I- FUNCTION: Tachykynins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretegogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC -I- SUBCELLULAR LOCATION: Secreted.  
CC -I- TISSUE SPECIFICITY: Skin.  
CC -I- SIMILARITY: Belongs to the tachykinin family.  
DR InterPro; IPR002040; Tachy\_Neurokinin.  
DR InterPro; IPR008215; Tachykinin.  
DR Pfam; PF02202; Tachykinin; 1.  
DR SMART; SM00203; TK; 1.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
KW Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1  
FT MOD\_RES 11 11  
FT SEQUENCE 11 AA; 1252 MW; 32867C3E59CD457 CRC64;  
SQ

Query Match 36.0%; Score 18; DB 1; Length 11;  
Best Local Similarity 75.0%; Pred. No. 1.1e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PDEN 6  
| : |  
2 PDPN 5

## RESULT 16

TKN2\_PSEGU STANDARD; PRT; 11 AA.  
AC P42987;  
DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Kassinin-like peptide K-II (Pg-KII).  
 OS Pseudophryne guentheri (Guenther's toadlet).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Myobatrachidae;  
 CC Myobatrachinae; Pseudophryne.  
 OX NCBI\_TaxID=30349;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=90287814; PubMed=2356157;  
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
 RA Roberts J.D., Melchiorri P., Erspamer V.;  
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
 the Australian frog Pseudophryne guentheri.",  
 RL Peptides 11:299-304 (1990).  
 CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secreteagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Skin.  
 CC -1- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR: C60409; C60409.  
 DR InterPro: IPR002040; Tachy Neurokinin.  
 DR Pfam: PF008215; Tachykinin.  
 DR SMART: SM00203; TK.1.  
 DR PROSITE: PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyroglutamate carboxylic acid.  
 FT MOD\_RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1246 MW; 3A247C37C9CB1A7 CRC64;  
 Query Match 36.0%; Score 18; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 PDE 5  
 4 PDE 6  
 Db 4 PDE 6  
 RESULT 17  
 ID TKN5\_PSEGU STANDARD; PRT; 11 AA.  
 AC P42990;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Substance P-like peptide II (Pg-SPII).  
 OS Pseudophryne guentheri (Guenther's toadlet).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Myobatrachidae;  
 CC Myobatrachinae; Pseudophryne.  
 OX NCBI\_TaxID=30349;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=90287814; PubMed=2356157;  
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
 RA Roberts J.D., Melchiorri P., Erspamer V.;  
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
 the Australian frog Pseudophryne guentheri.",  
 RL Peptides 11:299-304 (1990).  
 CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secreteagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Skin.

CC -1- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR: F60409; F60409.  
 DR InterPro: IPR002040; Tachy Neurokinin.  
 DR Pfam: PF008215; Tachykinin.  
 DR SMART: SM00203; TK.1.  
 DR PROSITE: PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyroglutamate carboxylic acid.  
 FT MOD\_RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1293 MW; 3A247C2CC9CB1457 CRC64;  
 Query Match 36.0%; Score 18; DB 1; Length 11;  
 Best Local Similarity 57.1%; Pred. No. 1.1e+03;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 3 PDENFL 9  
 4 PNEPFL 10  
 Db 4 PNEPFL 10  
 RESULT 18  
 ID MARI\_ALTSP STANDARD; PRT; 14 AA.  
 AC P29399;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Marinstatin C-2 (Marinstatin C-1; Marinstatin D).  
 OS Alteromonas sp. (strain B-10-31).  
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;  
 CC Alteromonadaceae; Alteromonas.  
 OX NCBI\_TaxID=29456;  
 RN [1]  
 RP SEQUENCE, AND ACTIVE SITE.  
 RX MEDLINE=92176155; PubMed=1794974;  
 RA Takano R., Imada C., Kamei K., Hara S.;  
 RT "The reactive site of marinstatin, a proteinase inhibitor from  
 marine Alteromonas sp. B-10-31.",  
 RL J. Biochem. 110:855-858 (1991).  
 CC -1- FUNCTION: INHIBITS SUBSTITILIN, CHYMOTRYPSIN, AND ELASTASE, BUT  
 CC NOT TRYPSIN.  
 KW Serine protease inhibitor; Pyroglutamate carboxylic acid.  
 FT PEPTIDE 1 14 MARINOSTATIN C-2.  
 FT PEPTIDE 3 14 MARINOSTATIN C-1.  
 FT PEPTIDE 4 14 MARINOSTATIN D.  
 FT MOD\_RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.  
 FT ACT\_SITE 6 7 REACTIVE BOND.  
 SQ SEQUENCE 14 AA; 1644 MW; 6E7CEFP92EF32E44 CRC64;  
 Query Match 36.0%; Score 18; DB 1; Length 14;  
 Best Local Similarity 33.3%; Pred. No. 1.4e+03;  
 Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 RFPDEN 6  
 7 RYPSDD 12  
 Db 7 RYPSDD 12  
 RESULT 19  
 ID PARI\_PANRE STANDARD; PRT; 8 AA.  
 AC P41872;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Parnafamide-like neuropeptide p1 (SDNPLRF-amide).  
 OS Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
 CC Panagrolaimoidea; Panagrolaimidae; Panagrellus.  
 OX NCBI\_TaxID=6233;  
 RN [1]

RP SEQUENCE.  
 RA MEDLINE=93027659; PubMed=1408999;  
 RX Geary T.G., Price D.A., Bowman J.W., Winterrowd C.A., Mackenzie C.D.,  
 RA Garrison R.D., Williams J.F., Friedman A.R.;  
 RT "Two FMRFamide-like peptides from the free-living nematode  
 RT Panagrellus redivivus";  
 RL Peptides 13:209-214(1992).  
 CC -1- FUNCTION: Myoactive.  
 CC -1- TISSUE SPECIFICITY: Nerve cords and paired groups of cells located  
 CC caudally to the base of the pharynx.  
 CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)  
 CC family.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 8  
 SQ SEQUENCE 8 AA; 995 MW; C6D40729C4576AB5 CRC64;

Query Match 34.0%; Score 17; DB 1; Length 8;  
 Best Local Similarity 75.0%; Pred. No. 1.4e+05;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 DENE 7  
 |||  
 Db 2 DPNF 5

## RESULT 20

FAR2\_PANRE STANDARD; PRT; 9 AA.  
 ID FAR2\_PANRE  
 AC P41873;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE FMRFamide-like neuropeptide PF2 (SADPNFLRF-amide).  
 OS Panagrellus redivivus.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
 OC Panagrolaimidae; Panagrolaimidae; Panagrellus.  
 OX NCBI\_TaxID=6233;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=93027659; PubMed=1408999;  
 RA Geary T.G., Price D.A., Bowman J.W., Winterrowd C.A., Mackenzie C.D.,  
 RA Garrison R.D., Williams J.F., Friedman A.R.;  
 RT "Two FMRFamide-like peptides from the free-living nematode  
 RT Panagrellus redivivus";  
 RL Peptides 13:209-214(1992).  
 CC -1- FUNCTION: Myoactive.  
 CC -1- TISSUE SPECIFICITY: Nerve cords and paired groups of cells located  
 CC caudally to the base of the pharynx.  
 CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)  
 CC family.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 9  
 SQ SEQUENCE 9 AA; 1066 MW; DA0B0729C4576AAD CRC64;

Query Match 34.0%; Score 17; DB 1; Length 9;  
 Best Local Similarity 75.0%; Pred. No. 1.4e+05;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 DENE 7  
 |||  
 Db 3 DPNF 6

## RESULT 21

FAR4\_CALVO STANDARD; PRT; 9 AA.  
 ID FAR4\_CALVO  
 AC P41859;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Calliphora vomitoria (Blue blowfly).  
 OS Calliphora vomitoria (Blue blowfly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Cestrioidea;  
 OC Calliphoridae; Calliphora.  
 OX NCBI\_TaxID=27454;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE=Thoracic ganglion;  
 RX MEDLINE=9219611; PubMed=1549555;  
 RA Drove H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,  
 RA Rehfeld J.F., Thorpe A.;  
 RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2  
 RT neuropeptides (designated calliphorin) from the blowfly  
 RT Calliphora vomitoria";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).  
 CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)  
 CC family.  
 DR PIR: D41978; D41978.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 9  
 SQ SEQUENCE 9 AA; 1182 MW; 31730699CAB6D457 CRC64;

Query Match 34.0%; Score 17; DB 1; Length 9;  
 Best Local Similarity 40.0%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 3 PDENE 7  
 ||::|  
 Db 2 PNDPF 6

## RESULT 22

URAT\_HUMAN STANDARD; PRT; 10 AA.  
 ID URAT\_HUMAN  
 AC P34990;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Unknown protein from 2D-page of red blood cells (Spot 2D-006H0)  
 DE (Fragment).  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Brain; Cytochrome;  
 RA Golaz O., Hughes G.J., Frutiger S., Paquet N., Baistroch A.,  
 RA Paquall C., Sanchez J.-C., Tissot J.-D., Appel R.D., Walzer C.,  
 RA Balant L., Hochstrasser D.F.;  
 RL Submitted (FEB-1994) to Swiss-Prot.  
 CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
 CC protein is: 4.77, its MW is: 26 kDa.  
 DR SWISS-2DPAGE; P34990; HUMAN.  
 FT NON\_TER 10  
 SQ SEQUENCE 10 AA; 1161 MW; F72D82B9C44B1871 CRC64;

Query Match 34.0%; Score 17; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ENF 7  
 |||  
 Db 5 ENF 7

## RESULT 23

UXA6\_CHLTR STANDARD; PRT; 10 AA.  
 ID UXA6\_CHLTR  
 AC P38007;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Unknown protein from 2D-page from elementary body (Fragment).  
 OS Chlamydia trachomatis.

OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
 OX NCBI\_TaxID=813;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=12/34/Bu;  
 RA Bin L., Santucci A., Maggi B., Marzocchi B., Sanchez-Campillo M.,  
 RA Comanducci M., Christensen G., Birkelund S., Viret E., Ratti G.,  
 RA Pallini V.;  
 RL Submitted (SEP-1994) to Swiss-Prot.  
 CC -1- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 6.44, ITS MW IS: 38.6 kDa.  
 DR Siena-2DPAGE; P38007; -.  
 FT NON TER  
 SQ SEQUENCE 10 AA; 1243 MW; DAD39A33304B5339 CRC64;  
 QY  
 DB 6 NFK 8  
 2 NFK 4  
 Query Match 34.0%; Score 17; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 RESULT 24  
 COXA\_CANFA STANDARD; PRT; 11 AA.  
 ID COXA\_CANFA  
 AC P99501;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Cytochrome c oxidase polypeptide Va (EC 1.9.3.1) (Fragment).  
 GN COX5A.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Heart;  
 RX MEDLINE=98163340; PubMed=9504812;  
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;  
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of  
 RT dog heart proteins";  
 RL Electrophoresis 18:2795-2802(1997).  
 CC -1- FUNCTION: This is the heme A-containing chain of cytochrome c  
 CC oxidase, the terminal oxidase in mitochondrial electron transport.  
 CC -1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome  
 CC c + 2 H(2)O.  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.  
 CC -1- SIMILARITY: Belongs to the cytochrome c oxidase Va family.  
 DR HSC-2DPAGE; P99501; DOG.  
 DR InterPro; IPR003204; Cyt\_c-ox5A.  
 DR Pfam; PF02284; COX5A; 1.  
 KW Oxidoreductase; Heme; Mitochondrion; Inner membrane.  
 FT NON TER  
 SQ SEQUENCE 11 AA; 1274 MW; 910B35CB1AB1F5 CRC64;  
 QY  
 DB 4 DENF 7  
 8 DEEF 11  
 Query Match 34.0%; Score 17; DB 1; Length 11;  
 Best Local Similarity 75.0%; Pred. No. 1.6e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 RESULT 25  
 UC04\_MAIZE STANDARD; PRT; 14 AA.  
 ID UC04\_MAIZE  
 AC P80610;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 128)  
 DS (Fragment).  
 OS Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACAD clade; Panicoideae; Andropogoneae; Zea.  
 OX NCBI\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Coleoptile;  
 RA Toulzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,  
 RA Pernollet J.-C., Zivy M., de Vienne D.;  
 RT "The maize two dimensional gel protein database: towards an integrated  
 RT genome analysis program";  
 RL Theor. Appl. Genet. 93:997-1005(1996).  
 CC -1- MISCELLANEOUS: On the 2D-gel the determined pi of this unknown  
 CC protein is: 6.8, its MW is: 34.6 kDa.  
 DR Maize-2DPAGE; P80610; COLEOPTILE.  
 FT NON TER  
 SQ SEQUENCE 14 AA; 1393 MW; C1451BA116D4AD CRC64;  
 QY  
 DB 4 DENF 7  
 2 DEGF 5  
 Query Match 34.0%; Score 17; DB 1; Length 14;  
 Best Local Similarity 75.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 RESULT 26  
 FAR1\_CALVO STANDARD; PRT; 9 AA.  
 ID FAR1\_CALVO  
 AC P41856;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Callifmrfamide 1.  
 OS Calliphora vomitoria (Blue blowfly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 OC Calliphoridae; Calliphora.  
 OX NCBI\_TaxID=27454;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Thoracic ganglion;  
 RX MEDLINE=92196111; PubMed=1549595;  
 RA Duvé H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,  
 RA Rehfeld J.F., Thorpe A.;  
 RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2  
 RT neuropeptides (designated callifmrfamides) from the blowfly  
 RT Calliphora vomitoria";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).  
 CC -1- FUNCTION: Able to induce fluid secretion from the isolated  
 CC salivary gland of Calliphora.  
 CC -1- SIMILARITY: Belongs to the FMRP (FMRamide related peptide)  
 CC family.  
 DR PIR; A41978; A41978.  
 KW Neuropeptide; Amidation.  
 FT MOD RES  
 SQ SEQUENCE 9 AA; 1169 MW; 29D00699CAB6C67 CRC64;  
 QY  
 DB 3 PDENF 7  
 2 PQQDF 6  
 Query Match 32.0%; Score 16; DB 1; Length 9;  
 Best Local Similarity 40.0%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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RESULT 27
FAR3 CALVO STANDARD; PRT; 9 AA.
ID FAR3 CALVO STANDARD; PRT; 9 AA.
AC P41857;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRamide 2.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea; Calliphoridae; Calliphora.
NCBI_TaxID=27454;
RN NCBI_TaxID=27454;
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=9219611; PubMed=1549595;
RA Duvé H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I., Reifeid J.F., Thorpe A.; and activity of -Phe-Met-Arg-Phe-NH2 neuropeptides (designated calliFMRamides) from the blowfly Calliphora vomitoria. Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2 neuropeptides (designated calliFMRamides) from the blowfly Calliphora vomitoria."
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -1- FUNCTION: Able to induce fluid secretion from the isolated salivary gland of Calliphora.
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide) family.
CC PIR; B41978; B41978.
DR Neuropeptide; Amidation.
KW MOD RES 9
FT MOD RES 9
SQ SEQUENCE 9 AA; 1128 MW; 29D00699CAB6C5A7 CRC64;

Query Match 32.0%; Score 16; DB 1; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 PDENF 7
| : : |
2 PSQDF 6

RESULT 28
FAR3 CALVO STANDARD; PRT; 9 AA.
ID FAR3 CALVO STANDARD; PRT; 9 AA.
AC P41858;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRamide 3.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea; Calliphoridae; Calliphora.
NCBI_TaxID=27454;
RN NCBI_TaxID=27454;
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=9219611; PubMed=1549595;
RA Duvé H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I., Reifeid J.F., Thorpe A.; and activity of -Phe-Met-Arg-Phe-NH2 neuropeptides (designated calliFMRamides) from the blowfly Calliphora vomitoria. Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2 neuropeptides (designated calliFMRamides) from the blowfly Calliphora vomitoria."
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -1- FUNCTION: Able to induce fluid secretion from the isolated salivary gland of Calliphora.
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide) family.
CC PIR; B41978; B41978.
DR Neuropeptide; Amidation.
KW MOD RES 9
FT MOD RES 9
SQ SEQUENCE 9 AA; 1128 MW; 29D00699CAB6C5A7 CRC64;

Query Match 32.0%; Score 16; DB 1; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 PDENF 7
| : : |
2 PSQDF 6

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Query Match 32.0%; Score 16; DB 1; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 PDENF 7
| : : |
2 PSQDF 6

RESULT 29
FAR1 SARBU STANDARD; PRT; 9 AA.
ID FAR1 SARBU STANDARD; PRT; 9 AA.
AC P83350;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neb-FMRamide 1.
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea; Sarcophagidae; Sarcophaga.
NCBI_TaxID=7385;
RN NCBI_TaxID=7385;
RP SEQUENCE, AMIDATION, AND FUNCTION.
RC TISSUE=CNS;
RX MEDLINE=22342733; PubMed=12438685;
RA Meusen T., Mertens I., Clynen E., Baggerman G., Nichols R., Nachman R.J., Huybrechts R., De loof A., Schoofs L.; "Identification in Drosophila melanogaster of the invertebrate G protein-coupled FMRamide receptor."
RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).
CC -1- FUNCTION: Has modulatory actions at skeletal neuromuscular junctions.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide) family.
CC Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
KW MOD RES 1
FT MOD RES 1
SQ SEQUENCE 9 AA; 1155 MW; 2D810699CAB6C5A7 CRC64;

Query Match 32.0%; Score 16; DB 1; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 PDENF 7
| : : |
2 PSQDF 6

RESULT 30
FORB METTM STANDARD; PRT; 10 AA.
ID FORB METTM STANDARD; PRT; 10 AA.
AC P80901;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Pyruvate synthase subunit FORB (EC 1.2.7.1) (Pyruvate oxidoreductase beta chain) (FOR) (Pyruvate-ferredoxin oxidoreductase beta subunit) (Fragment).
DE POSB.
OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales; Methanobacteriaceae; Methanothermobacter.
NCBI_TaxID=79929;
RN NCBI_TaxID=79929;
RP SEQUENCE.
RX MEDLINE=97261844; PubMed=9108258;
RA Tersteegen A., Linder D., Thauer R.K., Hedderich R.; "Structures and functions of four anaerobic 2-oxoacid oxidoreductases in Methanobacterium thermoautotrophicum."
RL Eur. J. Biochem. 244:862-868(1997).

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CC -1- CATALYTIC ACTIVITY: Pyruvate + CoA + oxidized ferredoxin = acetyl-CoA + CO(2) + reduced ferredoxin.  
 CC -1- SUBUNIT: Heterotrimer of one alpha, one beta, one delta and one gamma chain.  
 CC -1- MISCELLANEOUS: Has a pH optimum of 10.0 and an optimal temperature of 80 degrees Celsius.  
 KM Oxidoreductase.  
 FT NON\_TER 10  
 SQ SEQUENCE 10 AA; 1232 MW; 167011DAF6DB0760 CRC64;

Query Match 32.0%; Score 16; DB 1; Length 10;  
 Best Local Similarity 40.0%; Pred. No. 2.3e+03;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 PDENF 7  
 DB 4 PEGXP 8

RESULT 31  
 PPCK\_FASHE STANDARD; PRT; 10 AA.  
 ID PPCK\_FASHE  
 AC P80525;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Putative phosphoenolpyruvate carboxylase (PEPCK) (EC 4.1.1.32)  
 DE (Phosphoenolpyruvate carboxylase)  
 DE protein 1 (Fragment).  
 OS Fasciola hepatica (Liver fluke).  
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;  
 OC Echinostomida; Echinostomata; Fasciolidae; Fasciola.  
 OX NCBI\_TaxID=6192;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=95366993; PubMed=7639732;  
 RA Tkalcic J., Asman K., Meusen E.;  
 RT "Fasciola hepatica: rapid identification of newly excysted juvenile proteins";  
 RL Biochem. Biophys. Res. Commun. 213:169-174(1995).  
 CC -1- CATALYTIC ACTIVITY: GTP + oxaloacetate = GDP + phosphoenolpyruvate + CO(2).  
 CC -1- SIMILARITY: Belongs to the phosphoenolpyruvate carboxylase (GTP) family.  
 CC InterPro: IPR008209; PEP carboxylin.  
 DR PROSITE: PS00505; PEPCK GTP; PARTIAL.  
 KW Lyase; Decarboxylase; GTP-binding.  
 FT NON\_TER 10  
 SQ SEQUENCE 10 AA; 1069 MW; 8393A6187AA9C87A CRC64;

Query Match 32.0%; Score 16; DB 1; Length 10;  
 Best Local Similarity 66.7%; Pred. No. 2.3e+03;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FPD 4  
 DB 1 YPD 3

RESULT 32  
 MPI\_MICOC STANDARD; PRT; 13 AA.  
 ID MPI\_MICOC  
 AC P81532;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE MPI protein (Fragments).  
 OS Microplitis ocellatae (Braconid wasp).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonidae;  
 OC Braconidae; Microgasterinae; Microplitis.  
 OX NCBI\_TaxID=99573;  
 RN [1]

RP SEQUENCE.  
 RA TISSUE=Larva;  
 RA Takahashi M.; Quicke D.L.J.;  
 RU Submitted (OCT-1998) to Swiss-Prot.  
 CC -1- TISSUE SPECIFICITY: Salivary glands.  
 CC -1- DEVELOPMENTAL STAGE: LARVAL.  
 FT NON\_CONS 10  
 SQ SEQUENCE 13 AA; 1595 MW; 0C0786C9DD82777B CRC64;

Query Match 32.0%; Score 16; DB 1; Length 13;  
 Best Local Similarity 33.3%; Pred. No. 3e+03;  
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDENF 7  
 DB 6 YPEVNV 11

RESULT 33  
 ATP6\_SPIOL STANDARD; PRT; 14 AA.  
 ID ATP6\_SPIOL  
 AC P80086;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE ATP synthase A chain (EC 3.6.3.14) (Protein 6) (Fragment).  
 GN ATP6.  
 OS Spinacia oleracea (Spinach).  
 OC Mitochondrion.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllales; Amaranthaceae; Spinacia.  
 OX NCBI\_TaxID=3562;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=cv. Medania; TISSUE=leaf mesophyll;  
 RX MEDLINE=92209531; PubMed=1113368;  
 RA Hamsaur B., Glaser E.;  
 RT "Plant mitochondrial F0F1 ATP synthase. Identification of the individual subunits and properties of the purified spinach leaf mitochondrial ATP synthase.";  
 RL Eur. J. Biochem. 205:409-416(1992).  
 CC -1- FUNCTION: Key component of the proton channel; it may play a direct role in the translocation of protons across the membrane.  
 CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate + H(+) (Out).  
 CC -1- SUBUNIT: F-type ATPases have 2 components, CF(1) - the catalytic core - and CF(0) - the membrane proton channel. CF(1) has five subunits: alpha(3), beta(3), gamma(1), delta(1), epsilon(1). CF(0) has three main subunits: a, b and c.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 DR PIR: S21247; S21247.  
 DR InterPro: IPR000568; ATPsyn\_Asub.  
 DR PROSITE: PS00449; ATPASE\_A; PARTIAL.  
 KW Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.  
 FT NON\_TER 14  
 SQ SEQUENCE 14 AA; 1619 MW; 9F1D6018F01CF45 CRC64;

Query Match 32.0%; Score 16; DB 1; Length 14;  
 Best Local Similarity 42.9%; Pred. No. 3.3e+03;  
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 PDENF 9  
 DB 2 PLEGPSI 8

RESULT 34  
 AL16\_CYDPO STANDARD; PRT; 8 AA.  
 ID AL16\_CYDPO  
 AC P82157;  
 DT 30-MAY-2000 (Rel. 39, Created)



DT 30-MAY-2000 (Rel. 39, last sequence update)  
 DT 30-MAY-2000 (Rel. 39, last annotation update)  
 DE Cydiaastatin 6.  
 OS Cydia pomonella (Coddling moth).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Lepidoptera; Lepidoptera; Glossata; Ditrysia;  
 OC Tortricidae; Tortricidae; Olethreutinae; Cydia.  
 OC NCBI\_TaxID=82600;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Larva;  
 RX MEDLINE=98054539; PubMed=9328229;  
 RA Duvé H., Johnsen A.H., Maestre J.-L., Scott A.G., Winstanley D.,  
 RA Davey M., East P.D., Thorpe A.;  
 RT "Lepidopteran peptides of the allatostatin superfamily."  
 RL Peptides 18:1301-1309(1997).  
 CC -1- SIMILARITY: Belongs to the allatostatin family.  
 KM Neuropeptide; Amidation.  
 FT MOD\_RES 8  
 SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;  
 QY Query Match 30.0%; Score 15; DB 1; Length 8;  
 Best Local Similarity 57.1%; Pred. No. 1.4e+05;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 PDENFKL 9  
 DB 2 PLYNFGI 8

RESULT 35  
 FARA\_CALVO STANDARD; PRT; 9 AA.  
 ID FARA\_CALVO  
 AC P41860;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, last sequence update)  
 DT 01-NOV-1995 (Rel. 32, last annotation update)  
 DE Calliphoridae 5.  
 OS Calliphora vomitoria (Blue blowfly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 OC Calliphoridae; Calliphora.  
 OC NCBI\_TaxID=27454;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Thoracic ganglion;  
 RX MEDLINE=92196111; PubMed=1549595;  
 RA Duvé H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,  
 RA Rehfeld J.F., Thorpe A.;  
 RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2  
 RT neuropeptides (designated calliphorin) from the blowfly  
 RT Calliphora vomitoria."  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).  
 CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)  
 CC family.  
 CC PIR: E41978; E41978.  
 KM Neuropeptide; Amidation.  
 FT MOD\_RES 9  
 SQ SEQUENCE 9 AA; 1066 MW; 39D10699CAB6867 CRC64;

QY Query Match 30.0%; Score 15; DB 1; Length 9;  
 Best Local Similarity 40.0%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 PDENF 7  
 DB 2 PGQDF 6

RESULT 36  
 FARA\_CALVO STANDARD; PRT; 9 AA.  
 ID FARA\_CALVO  
 AC P41865;

DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, last sequence update)  
 DT 01-NOV-1995 (Rel. 32, last annotation update)  
 DE Calliphoridae 10.  
 OS Calliphora vomitoria (Blue blowfly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 OC Calliphoridae; Calliphora.  
 OC NCBI\_TaxID=27454;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Thoracic ganglion;  
 RX MEDLINE=92196111; PubMed=1549595;  
 RA Duvé H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,  
 RA Rehfeld J.F., Thorpe A.;  
 RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2  
 RT neuropeptides (designated calliphorin) from the blowfly  
 RT Calliphora vomitoria."  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).  
 CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)  
 CC family.  
 CC PIR: A44787; A44787.  
 KM Neuropeptide; Amidation.  
 FT MOD\_RES 9  
 SQ SEQUENCE 9 AA; 1183 MW; 29D00699CAB40457 CRC64;

QY Query Match 30.0%; Score 15; DB 1; Length 9;  
 Best Local Similarity 40.0%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 PDENF 7  
 DB 2 PNRDF 6

RESULT 37  
 Q2OB\_COMTE STANDARD; PRT; 10 AA.  
 ID Q2OB\_COMTE  
 AC P80465;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, last sequence update)  
 DT 16-OCT-2001 (Rel. 40, last annotation update)  
 DE Quinolone 2-oxidoeductase, beta chain (EC 1.3.99.17) (Fragment).  
 OS Comamonas testosteroni (Pseudomonas testosteroni).  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Comamonadaceae; Comamonas.  
 OC NCBI\_TaxID=285;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=63;  
 RX MEDLINE=96035889; PubMed=7556204;  
 RA Schach S., Tshienaka B., Fetzner S., Jings F.,  
 RA "Quinolone 2-oxidoeductase and 2-oxo-1,2-dihydroquinoline 5,6-  
 RT dioxygenase from Comamonas testosteroni 63. The first two enzymes in  
 RT quinoline and 3-methylquinoline degradation."  
 RL Eur. J. Biochem. 232:556-544(1995).  
 CC -1- FUNCTION: Converts (3-methyl-)-quinoline to (3-methyl)-2-oxo-1,2-  
 CC dihydroquinoline.  
 CC -1- CATALYTIC ACTIVITY: Quinolone + acceptor + H(2)O = isoguinolin-  
 CC 1(2H)-one + reduced acceptor.  
 CC -1- COFACTOR: FAD, molybdenum and iron-sulfur.  
 CC -1- PATHWAY: Degradation of quinoline and (3-methyl)-quinoline; first  
 CC step.  
 CC -1- SUBUNIT: Heterohexamer of two alpha chains, two beta chains, and  
 CC two gamma chains (probable).  
 KM Oxidoreductase; Flavoprotein; FAD; Molybdenum.  
 FT NON\_TER 10  
 SQ SEQUENCE 10 AA; 1241 MW; C2E2C25D93CDCT69 CRC64;

QY Query Match 30.0%; Score 15; DB 1; Length 10;  
 Best Local Similarity 66.7%; Pred. No. 3.6e+03;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFP 3  
: 11  
DB 2 KFP 4

## RESULT 38

UPA2\_HUMAN STANDARD; PRT; 10 AA.

AC P30088;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Unknown protein from 2D-page of plasma (Spot 10) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Plasma;  
RA MEDLINE=93092937; PubMed=1459097;  
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,  
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,  
RA Hochstrasser D.F.;  
RT "Plasma protein map: an update by microsequencing."  
RL Electrophoresis 13:707-714(1992)  
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
protein is: 4.4, its MW is: 49 KDa.  
DR SWISS-2DPAGE; P30088; HUMAN.  
FT NON\_TER  
FT UNSTURE  
FT NON\_TER  
SQ SEQUENCE 10 AA; 1079 MW; 51AC54AB7775B7 CRC64;

Query Match 30.0%; Score 15; DB 1; Length 10;  
Best Local Similarity 66.7%; Pred. No. 3.6e+03;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDE 5  
: 11  
DB 6 PDD 8

## RESULT 39

TKNA\_RANCA STANDARD; PRT; 11 AA.

ID TKNA\_RANCA  
AC P22688;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ranatichykinin A (RtK A).  
OS Rana catesbeiana (Bull frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.  
OX NCBI\_Taxid=8400;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RC TISSUE=Brain, and intestine;  
RA MEDLINE=9125437; PubMed=2041143;  
RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;  
RT "Isolation of four novel tachykinins from frog (Rana catesbeiana)  
brain and intestine."  
RL Biochem. Biophys. Res. Commun. 177:588-595(1991).  
RN [2]  
RP SEQUENCE.  
RC TISSUE=Intestine;  
RA MEDLINE=94023216; PubMed=8210506;  
RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;  
RT "Four novel tachykinins in frog (Rana catesbeiana) brain and  
intestine."  
RL Regul. Pept. 46:81-88(1993).  
CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,

CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: Belongs to the tachykinin family.

DR PIR; A61033; A61033.  
DR InterPro; IPR002040; Tachy\_Neurokinin.  
DR InterPro; IPR008215; Tachykinin.  
DR Pfam; PF02202; Tachykinin; 1.  
DR SMART; SM00203; TK; 1.  
DR PROSITE; PS00267; TACHYKININ; 1.  
DR Tachykinin; Neuropeptide; Amidation.  
FT MOD\_RES  
FT MOD\_RES  
SQ SEQUENCE 11 AA; 1311 MW; 200D60CC59D40AB7 CRC64;

Query Match 30.0%; Score 15; DB 1; Length 11;  
Best Local Similarity 42.9%; Pred. No. 3.9e+03;  
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 PDENFYL 9  
: 11  
DB 4 PDREYGL 10

## RESULT 40

PART\_CALVO STANDARD; PRT; 12 AA.

ID PART\_CALVO  
AC P41869;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Callimorphamide 1.  
OS Calliphora vomitoria (Blue blowfly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Calliphoridae; Calliphora.  
OX NCBI\_Taxid=27454;  
RN [1]  
RP SEQUENCE.

RC TISSUE=Thoracic ganglion;  
RA MEDLINE=92196111; PubMed=149595;  
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,  
RA Renfeld J.F., Thorpe A.;  
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2  
neuropeptides (designated callimorphamides) from the blowfly  
Calliphora vomitoria".  
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).  
CC -1- SIMILARITY: Belongs to the FMRP family (FMRP family related peptide)  
family.  
CC PIR; E44787; E44787.  
DR Neuropeptide; Amidation.  
FT MOD\_RES  
FT MOD\_RES  
SQ SEQUENCE 12 AA; 1390 MW; 2DDDB316914B5A7 CRC64;

Query Match 30.0%; Score 15; DB 1; Length 12;  
Best Local Similarity 50.0%; Pred. No. 4.3e+03;  
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 PDEN 6  
: 11  
DB 5 PSDN 8

## RESULT 41

TKN1\_KASMA STANDARD; PRT; 12 AA.

ID TKN1\_KASMA  
AC P08613;  
DT 01-AUG-1988 (Rel. 08, Created)  
DT 01-AUG-1988 (Rel. 08, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Hylambates kassinin ([Glu2,Pro5]kassinin).  
OS Kassina maculata (African rhacophorid frog) (Hylambates maculatus).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Hyperoliidae;  
 CC Kassina.  
 CC NCBI\_TaxID=8414;  
 RN [1]  
 RP SEQUENCE  
 RC TISSUE=Skin secretion;  
 RA Yasuhara T., Nakajima T., Erespamer G.F., Erespamer V.;  
 RT "New tachykinins, Glu2, Pro5-kassinin (hyalambates-kassinin) and  
 RT hyalambatin, in the skin of the African rhacophorid frog Hyalambates  
 RT maculatus";  
 RL Biomed. Res. 2:613-617(1981).  
 CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Skin.  
 CC -1- SIMILARITY: Belongs to the tachykinin family.  
 CC PIR: S10059; S10059.  
 CC InterPro: IPR02040; Tachy\_Neurokinin.  
 CC InterPro: IPR008215; Tachykinin.  
 CC Pfam: PF02202; Tachykinin; 1.  
 CC SMART: SM00203; TK; 1.  
 CC PROSITE: PS00267; TACHYKININ; 1.  
 CC Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation.  
 KM MOD\_RES 12 12 AMIDATION.  
 FT MOD\_RES 12 12  
 SQ SEQUENCE 12 AA; 1376 MW; 3E756D279DD6DAB7 CRC64;  
 QY Query Match 30.0%; Score 15; DB 1; Length 13;  
 Db Best Local Similarity 66.7%; Pred. No. 4.3e+03;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 PDE 5  
 Db 5 PDQ 7  
 RESULT 42  
 ADFB\_TENMO STANDARD; PRT; 13 AA.  
 ID ADFB\_TENMO  
 AC P83109;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Antidiuretic factor B (ADFB).  
 OS Tenebrio molitor (Yellow mealworm).  
 OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;  
 OC Tenebrionidae; Tenebrio.  
 CC NCBI\_TaxID=7067;  
 RN [1]  
 RP SEQUENCE, FUNCTION, TISSUE SPECIFICITY, MASS SPECTROMETRY, AND  
 RP SYNTHESIS.  
 RC TISSUE=Head;  
 RX MEDLINE=22465067; PubMed=12576082;  
 RA Eigenheer R.A., Wiehart U.M., Nicolson S.W., Schoofs L., Schegg K.M.,  
 RA Hull J.J., Schooley D.A.;  
 RT "Isolation, identification and localization of a second beetle  
 RT antidiuretic peptide";  
 RL Peptides 24:27-34(2003).  
 CC -1- FUNCTION: Inhibitor of fluid secretion by Malpighian tubules. Uses  
 CC CGMP as second messenger. May function as an antidiuretic  
 CC hormone.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Brain. Appears to be mainly expressed in two  
 CC pairs of bilaterally symmetrical cells in the protocerebrum.  
 CC -1- MASS SPECTROMETRY: MW=1560.33; METHOD=MALDI.  
 CC Neuropeptide; Hormone.  
 KM SEQUENCE 13 AA; 1562 MW; 0240A4504B8A632B CRC64;  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 13 AA; 1562 MW; 0240A4504B8A632B CRC64;  
 QY Query Match 30.0%; Score 15; DB 1; Length 13;  
 Db Best Local Similarity 28.6%; Pred. No. 4.7e+03;  
 Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 PDENFK 8  
 Db 1 YDDGSYK 7  
 RESULT 43  
 LPAA\_PORGI STANDARD; PRT; 13 AA.  
 ID LPAA\_PORGI  
 AC P81411;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Lipid A-associated protein (Fragment).  
 OS Porphyromonas gingivalis (Bacteroides gingivalis).  
 OS Bacteri; Bacteroidetes; Bacteroides (class); Bacteroidales;  
 OC Porphyromonadaceae; Porphyromonas.  
 CC NCBI\_TaxID=837;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=MS0;  
 RX MEDLINE=99061194; PubMed=9846737;  
 RA Curtis M., Henderson B., Tabona P.,  
 RA Sharp L., Peole S., Reddi K., Fletcher J., Nair S., Wilson M.,  
 RT "A lipid A-associated protein of Porphyromonas gingivalis, derived  
 RT from the haemagglutinating domain of the RI protease gene family, is  
 RT a potent stimulator of interleukin 6 synthesis";  
 RL Microbiology 144:3019-3026(1998).  
 CC -1- FUNCTION: IS ASSOCIATED WITH LIPID A, A PHOSPHORYLATED GLYCOLIPID  
 CC THAT ANCHORS THE LIPOLYSACCHARIDE TO THE OUTER MEMBRANE OF THE  
 CC CELL.  
 CC VARIANT 12 12 G -> F.  
 FT NON TER 13 13  
 FT MOD\_RES 13 13  
 SQ SEQUENCE 13 AA; 1346 MW; 38EA796EAF63AB7 CRC64;  
 QY Query Match 30.0%; Score 15; DB 1; Length 13;  
 Db Best Local Similarity 50.0%; Pred. No. 4.7e+03;  
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 PDEN 6  
 Db 6 PDKD 9  
 RESULT 44  
 LCK3\_LEUMA STANDARD; PRT; 8 AA.  
 ID LCK3\_LEUMA  
 AC P21142;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Leucokinin III (L-III).  
 OS Leucophaea maderae (Madaira cockroach).  
 OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidae;  
 CC Blaberidae; Leucophaea.  
 CC NCBI\_TaxID=6988;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Head;  
 RA Holman G.M., Cook B.J., Nachman R.U.;  
 RT "Primary structure and synthesis of two additional neuropeptides  
 RT from Leucophaea maderae: members of a new family of  
 RT cephalomyotrogins";  
 RL Comp. Biochem. Physiol. 84C:271-276(1986).  
 CC -1- FUNCTION: This cephalomyotrophic peptide stimulates contractile  
 CC activity of cockroach proctoderm (hindgut).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC Neuropeptide; Amidation.  
 KM MOD\_RES 8 8  
 FT MOD\_RES 8 8  
 SQ SEQUENCE 8 AA; 910 MW; DC6365B449C866DA CRC64;  
 QY Query Match 28.0%; Score 14; DB 1; Length 8;  
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Best Local Similarity 50.0%; Pred. No. 1.4e+05;  
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 DENE 7  
| : |  
Db 1 DOGF 4

## RESULT 45

SAMP MUSCA STANDARD; PRT; 9 AA.  
ID SAMP MUSCA STANDARD; PRT; 9 AA.  
AC P19095;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Serum amyloid P-component (SAP) (Fragment).  
OS Musculus canis (smooth dogfish).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes; Triakidae;  
OC Mustelus.  
OX NCBI\_TaxID=7812;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=83160932; PubMed=6403520;  
RA Robey F.A., Tanaka T., Liu T.-Y.;  
RT "Isolation and characterization of two major serum proteins from the  
RT dogfish, *Musculus canis*, C-reactive protein and amyloid P  
RT component.";  
RL J. Biol. Chem. 258:3889-3894(1983).  
CC -1- SUBUNIT: Homopentamer. Pentaxin (or pentraxin) have a discoid  
CC arrangement of 5 noncovalently bound subunits.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- DISEASE: SAP IS A PRECURSOR OF AMYLOID COMPONENT P WHICH IS FOUND  
CC IN BASEMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.  
CC -1- SIMILARITY: Belongs to the pentaxin family.  
DR PIR: B20569; B20569. Pentaxin.  
DR InterPro: IPR001759; Pentaxin.  
DR PROSITE: PS00289; PENTAXIN; PARTIAL.  
DR Lectin; Amyloid; Glycoprotein; Plasma; Pentaxin.  
KW DOMAIN  
FT DOMAIN 1  
FT NON TER 9  
SQ SEQUENCE 9 AA; 965 MW; D05B5735B3386769 CRC64;

Query Match 28.0%; Score 14; DB 1; Length 9;  
Best Local Similarity 40.0%; Pred. No. 1.4e+05;  
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PPDEN 6  
| : |  
Db 2 PPKS 6

Search completed: August 30, 2004, 10:50:23  
Job time : 2.55068 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2004, 10:41:54 / Search time 2.70608 Seconds  
(without alignments)  
319.918 Million cell updates/sec

Title: US-09-720-469a-7  
Perfect score: 50  
Sequence: 1 RPPDENFKL 9

Scoring table: BLOSUM62  
Gapcp 10.0, Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 1638

Minimum DB seq length: 8  
Maximum DB seq length: 14

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database: PIR 78:  
1: PIR1:  
2: PIR2:  
3: PIR3:  
4: PIR4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	46.0	11	2	E60409
2	20	40.0	13	2	S29488
3	20	40.0	14	2	A42473
4	20	40.0	14	2	S58862
5	20	40.0	14	2	S58866
6	20	40.0	14	2	PH1757
7	20	40.0	14	2	PH1758
8	20	40.0	14	2	PH1759
9	20	40.0	14	2	PH1766
10	20	40.0	14	2	PH1767
11	20	40.0	14	2	PH1768
12	20	40.0	14	2	PH1769
13	19	38.0	10	2	A60476
14	18	36.0	8	2	PH1407
15	18	36.0	8	2	A39892
16	18	36.0	9	2	S10784
17	18	36.0	9	2	B35710
18	18	36.0	10	2	PQ0753
19	18	36.0	11	2	F60409
20	18	36.0	11	2	B60409
21	18	36.0	11	2	S60409
22	18	36.0	11	2	S07203
23	18	36.0	14	2	A54370
24	17	34.0	9	2	G58502
25	17	34.0	9	2	D41978
26	17	34.0	10	2	A61354
27	17	34.0	11	2	J02307
28	17	34.0	12	2	A61309
29	17	34.0	12	2	A56878

30	17	34.0	12	2	PH1462	T-cell receptor be
31	17	34.0	14	2	A41589	25K elastin-bindin
32	16	32.0	9	2	A41978	callitricumamide 1 -
33	16	32.0	9	2	B41978	callitricumamide 2 -
34	16	32.0	9	2	A41978	callitricumamide 3 -
35	16	32.0	9	2	B49712	ATP-binding protei
36	16	32.0	10	2	S19296	16K protein - poul
37	16	32.0	12	2	S15815	translation elonga
38	16	32.0	13	2	S47373	T-cell antigen rec
39	16	32.0	14	2	S21247	H+-transporting tw
40	16	32.0	14	2	S29209	avenin alpha-2 - O
41	16	32.0	14	2	S29632	xylin 1,4-beta-xy1
42	16	32.0	14	2	PS0371	hypothetical prote
43	15	30.0	8	2	A46306	spasmodic toxin
44	15	30.0	8	2	A14683	aspartate transami
45	15	30.0	8	2	S29272	tocopherol-binding

## ALIGNMENTS

## RESULT 1

E60409  
substance P-like peptide I - frog (Pseudophryne guentheri)  
C/Species: Pseudophryne guentheri  
C/Date: 30-Jan-1993 #sequence\_revision 30-Jan-1993 #text\_change 02-Sep-2000  
C/Accession: E60409  
R/Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior  
Peptides 11, 299-304, 1990  
A/Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Australia.  
A/Reference number: A60409; PMID:90287814; PMID:2356157  
A/Accession: E60409  
A/Molecule type: protein  
A/Residues: 1-11 <SIM>  
C/Superfamily: unassigned animal peptides  
C/Keywords: amidated carboxyl end; pyroglutamic acid  
F/1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental  
F/1/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 46.0%; Score 23; DB 2; Length 11;  
Best Local Similarity 71.4%; Pred. No. 2.2e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 PDENFKL 9  
DB 4 PDEFGL 10

## RESULT 2

S29488  
GTP-binding protein o-rab3 - marbled electric ray (fragment)  
C/Species: Torpedo marmorata (marbled electric ray)  
C/Date: 22-Nov-1993 #sequence\_revision 27-Feb-1997 #text\_change 13-Mar-1997  
R/Volkandt, W.; Pevenier, J.; Elferink, L.A.; Scheller, R.H.  
FEBS Lett. 317, 53-56, 1993  
A/Title: Association of three small GTP-binding proteins with cholinergic synaptic vesic  
A/Reference number: S29485; PMID:93154521; PMID:8428654  
A/Accession: S29488  
A/Status: Preliminary  
A/Molecule type: protein  
A/Residues: 1-13 <VOL>

Query Match 40.0%; Score 20; DB 2; Length 13;  
Best Local Similarity 75.0%; Pred. No. 1e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DENF 7  
DB 5 DONF 8

## RESULT 3



PH1759  
T cell receptor alpha chain V region (clone IV alpha 7.2-3) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C/Accession: PH1759  
R/Portcell: S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.  
J. Exp. Med. 178, 1-16, 1993  
A/Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A/Reference number: PH1754; MUID:93301585; PMID:8391057  
A/Accession: PH1759  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-14 <POR>

Query Match  
Best Local Similarity 40.0%; Score 20; DB 2; Length 14;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 DENFKL 9  
DB 6 DSNYQL 11

RESULT 9  
PH1766  
T cell receptor alpha chain V region (clone 2V alpha 7.2-1) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C/Accession: PH1766  
R/Portcell: S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.  
J. Exp. Med. 178, 1-16, 1993  
A/Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A/Reference number: PH1754; MUID:93301585; PMID:8391057  
A/Accession: PH1766  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-14 <POR>

Query Match  
Best Local Similarity 40.0%; Score 20; DB 2; Length 14;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 DENFKL 9  
DB 6 DSNYQL 11

RESULT 10  
PH1767  
T cell receptor alpha chain V region (clone 2V alpha 7.2-2) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C/Accession: PH1767  
R/Portcell: S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.  
J. Exp. Med. 178, 1-16, 1993  
A/Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A/Reference number: PH1754; MUID:93301585; PMID:8391057  
A/Accession: PH1767  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-14 <POR>

Query Match  
Best Local Similarity 40.0%; Score 20; DB 2; Length 14;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 DENFKL 9  
DB 6 DSNYQL 11

RESULT 11  
PH1768  
T cell receptor alpha chain V region (clone 2V alpha 7.2-3) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C/Accession: PH1768  
R/Portcell: S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.  
J. Exp. Med. 178, 1-16, 1993  
A/Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A/Reference number: PH1754; MUID:93301585; PMID:8391057  
A/Accession: PH1768  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-14 <POR>

Query Match  
Best Local Similarity 40.0%; Score 20; DB 2; Length 14;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 DENFKL 9  
DB 6 DSNYQL 11

RESULT 12  
PH1769  
T cell receptor alpha chain V region (clone 2V alpha 7.2-4) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C/Accession: PH1769  
R/Portcell: S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.  
J. Exp. Med. 178, 1-16, 1993  
A/Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A/Reference number: PH1754; MUID:93301585; PMID:8391057  
A/Accession: PH1769  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-14 <POR>

Query Match  
Best Local Similarity 40.0%; Score 20; DB 2; Length 14;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 DENFKL 9  
DB 6 DSNYQL 11

RESULT 13  
A60476  
S-layer protein - Bacillus thuringiensis (fragment)  
C/Species: Bacillus thuringiensis  
C/Date: 20-Feb-1993 #sequence\_revision 20-Feb-1993 #text\_change 12-Mar-1993  
C/Accession: A60476  
R/Luckevich, M.D.; Beveridge, T.J.  
J. Bacteriol. 171, 6656-6667, 1989  
A/Title: Characterization of a dynamic S layer on Bacillus thuringiensis.  
A/Reference number: A60476; MUID:90078111; PMID:2592346  
A/Accession: A60476  
A/Molecule type: Protein  
A/Residues: 1-10 <LUC>  
C/Comment: The S-layer, or surface array, is the outermost component of several archaea

Query Match  
Best Local Similarity 38.0%; Score 19; DB 2; Length 10;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FPD 4  
DB 5 FPD 7

## RESULT 14

PH1407  
Ig heavy chain V region (Clone micro m+ 46-6 PCR) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 17-Mar-1999  
C/Accession: PH1407  
R/Shitrasawa, T.; Miyaoe, I.; Hagiwara, S.; Kimoto, H.; Shigemoto, K.; Taniguchi, M.; Takai, T.; Exp. Med. 176, 1209-1214, 1992  
A/Title: Heavy chain variable (VH) region diversity generated by VH gene replacement in a virus.  
A/Reference number: PH1403; MUID:93018837; PMID:1402663  
A/Accession: PH1407  
A/Molecule type: DNA  
A/Residues: 1-8 <SHI>  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin

Query Match  
Best Local Similarity 36.0%; Score 18; DB 2; Length 8;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFP 3  
|||  
DB 6 RFP 8

## RESULT 15

A39892  
P element, P cytotype-determining - fruit fly (Drosophila melanogaster) (fragment)  
C/Species: Drosophila melanogaster  
C/Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 16-Feb-1997  
C/Accession: A39892  
R/Nitasaki, E.; Mukai, T.; Yamazaki, T.  
Proc. Natl. Acad. Sci. U.S.A. 84, 7605-7608, 1987  
A/Title: Repressor of P elements in Drosophila melanogaster: cytotype determination by a  
A/Reference number: A39892  
A/Accession: A39892  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-8 <NIT>  
C/Genetics:  
A/Gene: FlyBase:P-element  
A/Cross-references: FlyBase:FBgn0003055

Query Match  
Best Local Similarity 36.0%; Score 18; DB 2; Length 8;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 ENFK 8  
|||  
DB 3 KNFK 6

## RESULT 16

S10784  
enamelin 1 - bovine (fragment)  
C/Species: Bos primigenius taurus (cattle)  
C/Date: 19-Mar-1997 #sequence\_revision 21-Nov-1998 #text\_change 21-Nov-1998  
C/Accession: S10784  
R/Strawich, E.; Glimcher, M.J.  
Eur. J. Biochem. 191, 47-56, 1990  
A/Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is albu  
A/Reference number: S10780; MUID:90336641; PMID:2379503  
A/Accession: S10784  
A/Molecule type: protein  
A/Residues: 1-9 <STR>  
C/Keywords: enamel; phosphoprotein

Query Match  
Best Local Similarity 36.0%; Score 18; DB 2; Length 9;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDENF 7  
|||  
DB 1 FPDGPF 6

## RESULT 17

B33710  
ornithine decarboxylase leader peptide - rat  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 27-Feb-1990 #sequence\_revision 27-Feb-1990 #text\_change 24-Sep-1999  
C/Accession: B33710  
R/Men, L.; Huang, J.K.; Blackshear, P.J.  
J. Biol. Chem. 264, 9016-9021, 1989  
A/Title: Rat ornithine decarboxylase gene. Nucleotide sequence, potential regulatory elen  
A/Reference number: A33710; MUID:89255378; PMID:2722815  
A/Accession: B33710  
A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
A/Molecule type: mRNA  
A/Residues: 1-10 <MEN>  
A/Cross-references: GB:J04791; NID:9205807; PIDN:AAA66163.1; PID:9806309  
C/Superfamily: unassigned leader peptides

Query Match  
Best Local Similarity 36.0%; Score 18; DB 2; Length 10;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFP 3  
|||  
DB 6 RFP 8

## RESULT 18

PQ0753  
beta-fructofuranosidase (BC 3.2.1.26) IIB - barley (fragment)  
C/Species: Hordeum vulgare (barley)  
C/Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 23-Mar-1995  
C/Accession: PQ0753  
R/Oberland, D.M.; Simmen, U.; Bolter, T.; Wiemken, A.  
Plant Physiol. 101, 1331-1339, 1993  
A/Title: Purification and characterization of three soluble invertases from barley (Horde  
A/Reference number: PQ0752; MUID:94143483; PMID:8310063  
A/Accession: PQ0753  
A/Molecule type: protein  
A/Residues: 1-10 <OBE>  
A/Experimental source: leaf, cv. Express  
C/Keywords: alternative initiators; glycoprotein; glycosidase; hydrolase

Query Match  
Best Local Similarity 36.0%; Score 18; DB 2; Length 10;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 FPDENFKL 9  
|||  
DB 2 FPDNTTML 9

## RESULT 19

F60409  
substance P-like peptide II - frog (Pseudophryne guentheri)  
C/Species: Pseudophryne guentheri  
C/Date: 30-Jan-1993 #sequence\_revision 30-Jan-1993 #text\_change 02-Sep-2000  
C/Accession: F60409  
R/Stimaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior  
Peptides 11, 299-304, 1990  
A/Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austral  
A/Reference number: F60409; MUID:90287814; PMID:2356157  
A/Accession: F60409  
A/Molecule type: protein  
A/Residues: 1-11 <SIM>  
C/Superfamily: unassigned animal peptides  
C/Keywords: amidated carboxyl end; pyroglutamic acid  
F1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental



F:11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 36.0%; Score 18; DB 2; Length 11;  
Best Local Similarity 57.1%; Pred. No. 2.1e+03;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 PDENFKL 9  
|||  
Db 4 PNEPFG 10

## RESULT 20

B60409  
kassinin-like peptide K-I - frog (Pseudophryne guentheri)

C:Species: Pseudophryne guentheri  
C>Date: 30-Jan-1993 #sequence\_revision 30-Jan-1993 #text\_change 18-Aug-2000

C:Accession: B60409  
R:Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior

A:Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austro

A:Reference number: A60409; PMID:90287814; PMID:2356157

A:Accession: B60409  
A:Molecule type: protein

A:Residues: 1-11 <SIM>  
A>Note: this peptide was also found in a deamidated form

C:Superfamily: unassigned animal peptides  
C:Keywords: amidated carboxyl end; pyroglutamic acid

F:11/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 36.0%; Score 18; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDE 5  
|||  
Db 4 PDE 6

## RESULT 21

C60409  
kassinin-like peptide K-II - frog (Pseudophryne guentheri)

C:Species: Pseudophryne guentheri  
C>Date: 30-Jan-1993 #sequence\_revision 30-Jan-1993 #text\_change 18-Aug-2000

C:Accession: C60409  
R:Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior

A:Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austro

A:Reference number: A60409; PMID:90287814; PMID:2356157

A:Accession: C60409  
A:Molecule type: protein

A:Residues: 1-11 <SIM>  
A>Note: this peptide was also found in a deamidated form

C:Superfamily: unassigned animal peptides  
C:Keywords: amidated carboxyl end; pyroglutamic acid

F:11/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 36.0%; Score 18; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDE 5  
|||  
Db 4 PDE 6

## RESULT 22

S07203  
uperolein - frog (Uperoleia marmorata)

C:Species: Uperoleia marmorata  
C>Date: 12-Feb-1993 #sequence\_revision 12-Mar-1993 #text\_change 18-Aug-2000

C:Accession: S07203

R:Anastasi, A.; Erspamer, V.; Eudean, R.

Experientia 31, 394-395, 1975

A:Title: Structure of uperolein, a physalaemin-like endocapeptide occurring in the skin of

A:Reference number: S07203; PMID:75131227; PMID:1120493

A:Accession: S07203  
A:Molecule type: protein

A:Residues: 1-11 <ANA>  
A:Superfamily: unassigned animal peptides

C:Keywords: amidated carboxyl end; pyroglutamic acid; skin; tachykinin

F:11/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 36.0%; Score 18; DB 2; Length 11;  
Best Local Similarity 75.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PDEN 6  
|||  
Db 2 PDEN 5

RESULT 23  
A54370  
inorganic diphosphatase (EC 3.6.1.1) - cucurbit (fragment)

C:Species: Cucurbita sp. (cucurbit)

C>Date: 07-Jul-1995 #sequence\_revision 07-Jul-1995 #text\_change 03-Jun-2002

C:Accession: A54370  
R:Sto, M.H.; Kaashara, M.; Ithil, N.; Homareda, H.; Matsui, H.; Yoshida, M.

A:Title: Purified vacuolar inorganic pyrophosphatase consisting of a 75-kDa polypeptide

A:Reference number: A54370; PMID:94165068; PMID:8120031

A:Accession: A54370  
A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-14 <SAT>  
A:Keywords: hydrolase

Query Match 36.0%; Score 18; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDE 5  
|||  
Db 11 PDE 13

RESULT 24  
G58502  
kidney and bladder stone protein - unidentified bacterium (fragment)

C:Species: unidentified bacterium

C>Date: 07-Feb-1997 #sequence\_revision 07-Feb-1997 #text\_change 10-Jul-1998

C:Accession: G58502  
R:Binette, J.P.; Binette, M.B.

A:Title: Submitted to the Protein Sequence Database, October 1996

A:Description: The proteins of kidney and gallbladder stones.

A:Reference number: A58501

A:Accession: G58502  
A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-9 <BIN>  
A:Experimental source: human kidney stone, bladder stone

A>Note: a secondary sequence AAKENPXD was also found

Query Match 34.0%; Score 17; DB 2; Length 9;  
Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 PDEN 7  
|||  
Db 3 PDVXF 7

## RESULT 25

D41978  
calliFMRamide 4 - bluebottle fly (Calliphora vomitoria)  
C/Species: Calliphora vomitoria  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 17-Mar-1999  
C/Accession: D41978  
R/Dave, H.; Johnson, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorpe  
Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992  
A/Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (desi  
A/Reference number: A41978; MUID:92196111; PMID:1549595  
A/Accession: D41978  
A/Status: Preliminary  
A/Molecule type: Protein  
A/Residues: 1-9 <DUV>  
C/Keywords: amidated carboxyl end; neuropeptide  
F/9/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 34.0%; Score 17; DB 2; Length 9;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDENF 7  
|:|:|  
DB 2 PNDPF 6

RESULT 26  
A61354  
carnitine medium/long chain acyltransferase (EC 2.3.1.-) - rat (fragment)  
N/Alternate names: endoplasmic reticulum protein ERp61; glucose regulated protein GRP58;  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-May-1999  
C/Accession: A61354  
R/Murthy, M.S.R.; Pande, S.V.  
Mol. Cell. Biochem. 122, 133-138, 1993  
A/Title: Carnitine medium/long chain acyltransferase of microsomes seems to be the previ  
A/Reference number: A61354; MUID:94049728; PMID:8222244  
A/Accession: A61354  
A/Status: Preliminary  
A/Molecule type: protein  
A/Residues: 1-10 <MUR>  
C/Keywords: acyltransferase

Query Match 34.0%; Score 17; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DEN 6  
|:|:|  
DB 8 DEN 10

RESULT 27  
JQ2307  
hypothetical 1.5K protein - tomato chloroplast (strain Toko)  
C/Species: chloroplast Lycopersicon esculentum (tomato)  
C/Date: 10-Mar-1994 #sequence\_revision 28-Oct-1994 #text\_change 23-Mar-1995  
C/Accession: JQ2307  
R/Kawagoe, Y.; Kikuta, Y.  
Theor. Appl. Genet. 81, 13-20, 1991  
A/Title: Chloroplast DNA evolution in potato (Solanum tuberosum L.).  
A/Reference number: JQ2306  
A/Accession: JQ2307  
A/Molecule type: DNA  
A/Residues: 1-11 <KAW>  
A/Experimental source: strain Toko  
C/Genetics:  
A/Genome: chloroplast  
C/Keywords: chloroplast

Query Match 34.0%; Score 17; DB 2; Length 11;  
Best Local Similarity 75.0%; Pred. No. 3.3e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 DENF 7  
|:|:|  
DB 5 DBEF 8

RESULT 28  
A61309  
glycoprotein hormones alpha chain - hamster (fragment)  
N/Alternate names: chorionodotrocin alpha chain; luteinizing hormone alpha chain; lutic  
C/Species: Cricetineae gen. sp. (hamster)  
C/Date: 17-Jul-1994 #sequence\_revision 17-Jul-1994 #text\_change 07-May-1999  
C/Accession: A61309  
R/Giem, S.D.; Nahm, H.S.; Greenwald, G.S.; Ward, D.N.  
Endocrinology 111, 1263-1269, 1982  
A/Title: Isolation and characterization of hamster luteinizing hormone.  
A/Reference number: A61309; MUID:83003498; PMID:6889489  
A/Accession: A61309  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-12 <GLB>  
C/Superfamily: glycoprotein hormones alpha chain  
C/Keywords: glycoprotein

Query Match 34.0%; Score 17; DB 2; Length 12;  
Best Local Similarity 28.6%; Pred. No. 3.6e+03;  
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 PDENFKL 9  
|:|:|  
DB 2 PBDFTM 8

RESULT 29  
A56878  
light yellow cell peptide A - great pond snail  
N/Contains: light yellow cell peptide B  
C/Species: Lymnaea stagnalis (great pond snail)  
C/Date: 11-Aug-1995 #sequence\_revision 11-Aug-1995 #text\_change 20-Aug-1999  
C/Accession: A56878  
R/Hoek, R.M.; Li, K.W.; van Minnen, J.; Geraerts, W.P.  
Brain Res. Mol. Brain Res. 16, 71-74, 1992  
A/Title: Chemical characterization of a novel peptide from the neuroendocrine light yell  
A/Reference number: A56878; MUID:9309519; PMID:1333202  
A/Accession: A56878  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-12 <HOE>  
A/Cross-references: PIDN:AAB2443.1; PID:9261422  
A/Note: sequence extracted from NCBI backbone (NCBIP:120090)  
C/Keywords: neuropeptide  
F/1-12/Product: light yellow cell peptide A #status experimental <YCPA>  
F/2-12/Product: light yellow cell peptide B #status experimental <YCPB>

Query Match 34.0%; Score 17; DB 2; Length 12;  
Best Local Similarity 42.9%; Pred. No. 3.6e+03;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 PDENFKL 9  
|:|:|  
DB 3 PDKSTIL 9

RESULT 30  
PH1462  
T-cell receptor beta chain (clone A24/PEF1) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 11-Apr-1995  
C/Accession: PH1462  
R/Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Ko  
J. Exp. Med. 177, 811-820, 1993  
A/Title: T cell receptor selection by and recognition of two class I major histocompatibi  
A/Reference number: PH1430; MUID:93171821; PMID:8436911  
A/Accession: PH1462

A:Molecule type: mRNA  
 A:Residues: 1-12 <CAS>  
 A:Experimental source: cytolytic T-lymphocyte  
 C:Superfamily: immunoglobulin homology  
 C:Keywords: receptor; T-cell

Query Match 34.0%; Score 17; DB 2; Length 12;  
 Best Local Similarity 60.0%; Pred. No. 3.6e+03;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 PDENF 7  
 |||  
 Db 7 PDYTF 11

RESULT 31  
 A41589  
 25K elastin-binding protein - Staphylococcus aureus (fragment)  
 C:Species: Staphylococcus aureus  
 C>Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 23-Mar-1993  
 C:Accession: A41589  
 R:Park, P.W.; Roberts, D.D.; Grosse, L.E.; Parke, W.C.; Rosenblom, J.; Abrams, W.R.; Mc  
 J. Biol. Chem. 266, 23399-23406, 1991  
 A:Title: Binding of elastin to Staphylococcus aureus.  
 A:Reference number: A41589; MUID:92078218; PMID:1744133  
 A:Accession: A41589  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-14 <PAR>

Query Match 34.0%; Score 17; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NFX 8  
 |||  
 Db 3 NFX 5

RESULT 32  
 A41978  
 calliphormamide 1 - bluebottle fly (Calliphora vomitoria)  
 C:Species: Calliphora vomitoria  
 C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 17-Mar-1999  
 C:Accession: A41978  
 R:Dive, H.; Johnsen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorpe  
 Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992  
 A:Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (desi  
 A:Reference number: A41978; MUID:92196111; PMID:1549595  
 A:Accession: A41978  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-9 <DUV>  
 C:Keywords: amidated carboxyl end; neuropeptide  
 F:9/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 32.0%; Score 16; DB 2; Length 9;  
 Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 PDENF 7  
 |||  
 Db 2 PQQDF 6

RESULT 33  
 B41978  
 calliphormamide 2 - bluebottle fly (Calliphora vomitoria)  
 C:Species: Calliphora vomitoria  
 C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 17-Mar-1999  
 C:Accession: B41978  
 R:Dive, H.; Johnsen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorpe  
 Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992

A:Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (desi  
 A:Reference number: A41978; MUID:92196111; PMID:1549595

A:Accession: B41978  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-9 <DUV>  
 C:Keywords: amidated carboxyl end; neuropeptide  
 F:9/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 32.0%; Score 16; DB 2; Length 9;  
 Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 PDENF 7  
 |||  
 Db 2 PQQDF 6

RESULT 34  
 C41978  
 calliphormamide 3 - bluebottle fly (Calliphora vomitoria)  
 C:Species: Calliphora vomitoria  
 C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 17-Mar-1999  
 C:Accession: C41978  
 R:Dive, H.; Johnsen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorpe,  
 Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992  
 A:Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (desi  
 A:Reference number: A41978; MUID:92196111; PMID:1549595  
 A:Accession: C41978  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-9 <DUV>  
 C:Keywords: amidated carboxyl end; neuropeptide  
 F:9/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 32.0%; Score 16; DB 2; Length 9;  
 Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 PDENF 7  
 |||  
 Db 2 PQQDF 6

RESULT 35  
 B49712  
 ATP-binding protein p46 - dog (fragment)  
 C:Species: Canis lupus familiaris (dog)  
 C>Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 07-May-1999  
 C:Accession: B49712  
 R:Nigam, S.K.; Goldberg, A.L.; Ho, S.; Rohde, M.F.; Bush, K.T.; Sherman, M.Y.  
 J. Biol. Chem. 269, 1744-1749, 1994  
 A:Title: A set of endoplasmic reticulum proteins possessing properties of molecular chap  
 A:Reference number: A49712; MUID:94124514; PMID:8294423  
 A:Accession: B49712  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-9 <NIG>  
 C:Keywords: ATP; endoplasmic reticulum; molecular chaperone

Query Match 32.0%; Score 16; DB 2; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FPD 4  
 |||  
 Db 5 YPD 7

RESULT 36  
 S19296  
 16K protein - pouliard wheat  
 C:Species: Triticum turgidum (pouliard wheat)

C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Jul-1997  
C/Accession: S19296  
R/Sanchez-Monge, R.; Gomez, L.; Barber, D.; Lopez-Otin, C.; Armentia, A.; Salcedo, G.  
Biochem. J. 281, 401-405, 1992  
A/Title: Wheat and barley allergens associated with baker's asthma. Glycosylated subunit  
A/Reference number: S19296; MUID:92143804; PMID:1736890  
A/Accession: S19296  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-10 <SN>

Query Match 32.0%; Score 16; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 4.7e+03;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDEN 6  
DB 3 PDQS 6

## RESULT 37

S15815  
translation elongation factor eEF-2 - rabbit (fragment)  
C/Species: Oryctolagus cuniculus (domestic rabbit)  
C/Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 18-Mar-1997  
C/Accession: S15815; S12970  
R/Price, N.T.; Redpath, N.T.; Severinov, K.V.; Campbell, D.G.; Russell, J.M.; Proud, C.G.  
FEBS Lett. 282, 253-258, 1991  
A/Title: Identification of the phosphorylation sites in elongation factor-2 from rabbit  
A/Reference number: S15815; MUID:91243806; PMID:2037042  
A/Accession: S15815  
A/Molecule type: protein  
A/Residues: 1-12 <OMP>  
R/Ovchinnikov, L.P.; Motuz, L.P.; Natapov, P.G.; Averbuch, L.J.; Wettenthal, R.E.H.; Szy  
FEBS Lett. 275, 209-212, 1990  
A/Title: Three phosphorylation sites in elongation factor 2.  
A/Reference number: S12970; MUID:91085562; PMID:2261989  
A/Accession: S12970  
A/Molecule type: protein  
A/Residues: 2-12 <OV>  
C/Superfamily: translation elongation factor 2; translation elongation factor Tu homolog  
C/Keywords: GTP binding; phosphoprotein; protein biosynthesis  
F/8,10/Binding site: phosphate (Thr) (covalent) (by elongation factor 2 kinase) #status

Query Match 32.0%; Score 16; DB 2; Length 12;  
Best Local Similarity 75.0%; Pred. No. 5.7e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RFPD 4  
DB 6 RFTD 9

## RESULT 38

S47373  
T-cell antigen receptor VJ junction beta chain - human  
C/Species: Homo sapiens (man)  
C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 05-Nov-1999  
C/Accession: S47373  
R/Lehner, P.J.  
submitted to the EMBL Data Library, August 1994  
A/Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T  
A/Reference number: S47355  
A/Accession: S47373  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-13 <LEH>  
A/Cross-references: EMBL:Z35672; NID:9527489; PIDN:CAA84741.1; PID:9527490  
C/Keywords: T-cell receptor

Query Match 32.0%; Score 16; DB 2; Length 13;  
Best Local Similarity 42.9%; Pred. No. 6.2e+03;  
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RFPDEN 7  
DB 6 RSDADEX 12

## RESULT 39

S21247  
H+-transporting two-sector ATPase (EC 3.6.3.14) protein 6 - spinach mitochondrion (fragme  
N/Alternate names: 18.5K protein  
C/Species: mitochondrion Spinacia oleracea (spinach)  
C/Date: 19-Mar-1997 #sequence\_revision 24-Mar-1999 #text\_change 03-Jun-2002  
C/Accession: S21247  
R/Hamasur, B.; Glaser, E.  
Eur. J. Biochem. 205, 409-416, 1992  
A/Title: Plant mitochondrial F(0)F(1) ATP synthase. Identification of the individual sub  
A/Reference number: S21204; MUID:92209531; PMID:131368  
A/Accession: S21247  
A/Molecule type: protein  
A/Residues: 1-14 <HAM>  
A/Experimental source: leaf  
C/Genetics:

A/Genome: mitochondrion  
C/Superfamily: H+-transporting ATP synthase protein 6  
C/Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; oxia

Query Match 32.0%; Score 16; DB 2; Length 14;  
Best Local Similarity 42.9%; Pred. No. 6.7e+03;  
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 PDENFKL 9  
DB 2 PLEQFSI 8

## RESULT 40

S29209  
avenin alpha-2 - oat (fragment)  
N/Alternate names: CIP-3; coeliac immunoreactive protein 3  
C/Species: Avena sativa (oat)  
C/Date: 19-Mar-1997 #sequence\_revision 24-Jul-1998 #text\_change 24-Jul-1998  
C/Accession: S29209  
R/Rocher, A.; Collilla, F.; Ortiz, M.L.; Mendez, E.  
FEBS Lett. 310, 37-40, 1992  
A/Title: Identification of the three major coeliac immunoreactive proteins and one alpha-  
A/Reference number: S29207; MUID:92405739; PMID:1526282  
A/Accession: S29209  
A/Molecule type: protein  
A/Residues: 1-14 <ROC>  
A/Experimental source: endosperm  
A/Superfamily: gliadin  
C/Keywords: prolamin; seed

Query Match 32.0%; Score 16; DB 2; Length 14;  
Best Local Similarity 33.3%; Pred. No. 6.7e+03;  
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 PDENFK 8  
DB 8 PSEQYO 13

## RESULT 41

S29632  
xylin 1,4-beta-xylosidase (EC 3.2.1.37) - Thermotoga sp. (strain FJSS3-B.1) (fragment)  
N/Alternate names: beta-xylosidase  
C/Species: Thermotoga sp.  
A/Variety: FJSS3-B.1  
C/Date: 19-Mar-1997 #sequence\_revision 24-Mar-1999 #text\_change 18-Jun-1999  
C/Accession: S29632  
R/Ruttermith, L.D.; Daniel, R.M.  
Biochim. Biophys. Acta 1156, 167-172, 1993  
A/Title: Thermostable beta-glucosidase and beta-xylosidase from Thermotoga sp. strain FJ

A:Reference number: S29631; MUID:93152594; PMID:8427876  
 A:Accession: S29632  
 A:Molecule type: protein  
 A:Residues: 1-14 <RUT>  
 A:Experimental source: strain F1S93-B.1  
 C:Comment: Although the beta-xylosidase enzyme activity was apparently confirmed for this  
 C:Function:  
 A:Description: hydrolyzes short chain oligosaccharides and xylobiose to produce D-xylose  
 A:Note: plays an important role in the relief of end-product inhibition of endoxylanase  
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 32.0%; Score 16; DB 2; Length 14;  
 Best Local Similarity 75.0%; Pred. No. 6.7e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PPDE 5  
 : : :  
 Db 8 FADE 11

## RESULT 42

PS0371  
 C:Species: Synechococcus sp. (fragment)  
 C:Date: 17-Aug-1992 #sequence\_revision 17-Aug-1992 #text\_change 08-Oct-1999  
 C:Accession: PS0371  
 R:Rhie, E.; Stirewalt, V.L.; Gasparich, G.E.; Bryant, D.A.  
 Gene 112, 123-128, 1992  
 A:Title: The pac genes of Synechococcus sp. PCC7002 and Cyanophora paradoxa: cloning an  
 A:Reference number: J50694; MUID:92201692; PMID:1551590  
 A:Accession: PS0371  
 A:Molecule type: DNA  
 A:Residues: 1-14 <RHT>  
 A:Cross-references: GB:M86238; NID:G154574; PID:AAA27351.1; PID:G552030

Query Match 32.0%; Score 16; DB 2; Length 14;  
 Best Local Similarity 60.0%; Pred. No. 6.7e+03;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 ENFKL 9  
 : : :  
 Db 2 KGFKL 6

## RESULT 43

A46306  
 C:Species: Phoneutria nigriventer (fragment)  
 C:Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 17-Mar-1999  
 C:Accession: A46306  
 R:Marangoni, S.; Borges, N.C.C.; Marangoni, R.A.; Antunes, E.; Vieira, C.A.; Novello, J.  
 Toxicon 31, 377-384, 1993  
 A:Title: Biochemical characterization of a vascular smooth muscle contracting polypeptide  
 A:Reference number: A46306; MUID:93276438; PMID:8503129  
 A:Accession: A46306  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-8 <MAR>

Query Match 30.0%; Score 15; DB 2; Length 8;  
 Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PPDEN 6  
 : : :  
 Db 3 PPGQS 7

## RESULT 44

A14683  
 C:Species: Gallus gallus (chicken)  
 A:Title: aspartate transaminase (EC 2.6.1.1), mitochondrial - chicken (tentative sequence) (fragm  
 N:Alternate names: aspartate aminotransferase, mitochondrial  
 C:Species: Gallus gallus (chicken)

C:Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 31-Mar-2000  
 C:Accession: A14683  
 R:Wilson, K.J.; Hunziker, P.; Hughes, G.J.  
 FEBS Lett. 108, 98-102, 1979

A:Title: Microsequence analysis: IV. Automatic liquid-phase sequencing using DABITC.  
 A:Reference number: A14683; MUID:800922116; PMID:520566  
 A:Accession: A14683  
 A:Molecule type: protein  
 A:Residues: 1-8 <WIL>  
 C:Keywords: aminotransferase; mitochondrion

Query Match 30.0%; Score 15; DB 2; Length 8;  
 Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 DENFK 8  
 : : :  
 Db 2 ENNFQ 6

## RESULT 45

S29272  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 22-Nov-1993 #sequence\_revision 12-Apr-1996 #text\_change 12-Apr-1996  
 C:Accession: S29272  
 R:Malecz, K.A.; Malecz, M.J.; Azzi, A.  
 Eur. J. Biochem. 209, 37-42, 1992  
 A:Title: Isolation of tocopherol-binding proteins from the cytosol of smooth muscle A7r5  
 A:Reference number: S29272; MUID:93011150; PMID:1396710  
 A:Accession: S29272  
 A:Molecule type: protein  
 A:Residues: 1-8 <NAL>  
 A:Experimental source: smooth muscle A7r5 cells

Query Match 30.0%; Score 15; DB 2; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDEN 6  
 : : :  
 Db 1 PEED 4

Search completed: August 30, 2004, 10:58:51  
 Job time : 2.70608 secs



Thu Sep 2 07:41:42 2004

US-09-720-469a-7.aug30.rapb

Page 1

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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:49:45 ; Search time 11.0068 Seconds

(without alignments)  
257.253 Million cell updates/sec

Title: US-09-720-469a-7  
Perfect score: 50  
Sequence: 1 RFPDENPKL 9

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1297172 seqs, 314612898 residues

Total number of hits satisfying chosen parameters: 149443

Minimum DB seq length: 8  
Maximum DB seq length: 14

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09C\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	60.0	9	16	US-10-264-309-118 Sequence 118, App
2	29	58.0	9	12	US-09-988-493-293 Sequence 293, App
3	29	58.0	9	12	US-10-014-340-209 Sequence 209, App
4	29	58.0	10	14	US-10-062-109A-328 Sequence 328, App
5	29	58.0	10	14	US-10-005-480A-328 Sequence 328, App
6	29	58.0	14	10	US-09-880-748-2437 Sequence 2437, App
7	29	58.0	14	10	US-09-880-748-2684 Sequence 2684, App
8	29	58.0	14	10	US-10-293-418-2837 Sequence 2837, App
9	29	58.0	14	12	US-10-293-418-2684 Sequence 2684, App
10	27	54.0	8	14	US-10-226-629A-464 Sequence 464, App
11	27	54.0	8	14	US-09-938-864-36 Sequence 36, App
12	27	54.0	9	10	US-09-938-864-36 Sequence 36, App
13	27	54.0	9	10	US-09-791-477-36 Sequence 36, App
14	27	54.0	9	10	US-09-785-019-36 Sequence 36, App
15	27	54.0	9	14	US-10-125-635A-36 Sequence 36, App

#### ALIGNMENTS

RESULT 1  
US-10-264-309-118  
; Sequence 118, Application US/10264309  
; Publication No. US20040022794A1  
; GENERAL INFORMATION:  
; APPLICANT: DUREAN, L. KATHRYN  
; APPLICANT: FRIEDMAN, DAVID L.  
; APPLICANT: HERATH, HERATH  
; APPLICANT: KIMBLE, LIDA H.  
; APPLICANT: PAREKH, RAJESH B.  
; APPLICANT: POTTER, DAVID M.  
; APPLICANT: ROHLER, CHRISTIAN  
; APPLICANT: SILBER, B. MICHAEL  
; APPLICANT: SNYDER, PETER J.  
; APPLICANT: SOARES, HOLLY D.  
; APPLICANT: STIGER, THOMAS R.  
; APPLICANT: SUNDERLAND, P. TREY  
; APPLICANT: TOWNSEND, ROBERT R.  
; APPLICANT: WHITE, W. FROST  
; APPLICANT: WILLIAMS, STEPHEN A.  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREOF,  
; INCLUDING DIAGNOSIS AND TREATMENT OF ALZHEIMER'S DISEASE  
; FILE REFERENCE: POA-002.01  
; CURRENT APPLICATION NUMBER: US/10/264,309  
; PRIOR FILING DATE: 2002-10-03  
; PRIOR FILING DATE: 2001-10-03  
; NUMBER OF SEQ ID NOS: 491  
; SOFTWARE: PatentIn Version 2.1  
; SEQ ID NO 118  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-264-309-118

Query Match 60.0%, Score 30, DB 16, Length 9,  
Best Local Similarity 75.0%, Pred. No. 1.2e+06,  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDENFKL 9  
| | | | |  
Db 1 FEDENFLL 8

## RESULT 2

US-09-988-493-293  
; Sequence 293, Application US/09988493  
; Publication No. US20030064419A1  
; GENERAL INFORMATION:  
; APPLICANT: Herath, Michael  
; APPLICANT: O'Hare, Michael John  
; APPLICANT: Page, Martin John  
; APPLICANT: Parekh, Rajesh Bhikhu  
; APPLICANT: Waterfield, Michael Derek  
; TITLE OF INVENTION: Proteins, Genes, and Their Use for  
; FILE REFERENCE: 2543-1-024  
; CURRENT APPLICATION NUMBER: US/09/988,493  
; PRIOR FILING DATE: 2002-05-21  
; PRIOR APPLICATION NUMBER: PCT/GB01/01219  
; PRIOR FILING DATE: 2001-03-20  
; PRIOR APPLICATION NUMBER: GB 0006695.1  
; PRIOR FILING DATE: 2000-03-20  
; PRIOR APPLICATION NUMBER: GB 0007265.2  
; NUMBER OF SEQ ID NOS: 308  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 293  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: homo sapien  
US-09-988-493-293

Query Match 58.0%; Score 29; DB 12; Length 9;  
Best Local Similarity 75.0%; Pred. No. 1.2e+06;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDENFKL 9  
| | | | |  
Db 1 FEDENFLL 8

## RESULT 3

US-10-014-340-209  
; Sequence 209, Application US/10014340  
; Publication No. US20030064411A1  
; GENERAL INFORMATION:  
; APPLICANT: Herath, et al  
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor, Including  
; FILE REFERENCE: 9195-078  
; CURRENT APPLICATION NUMBER: US/10/014,340  
; CURRENT FILING DATE: 2001-12-10  
; NUMBER OF SEQ ID NOS: 823  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 209  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-014-340-209

Query Match 58.0%; Score 29; DB 12; Length 9;  
Best Local Similarity 75.0%; Pred. No. 1.2e+06;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDENFKL 9  
| | | | |  
Db 1 FEDENFLL 8

## RESULT 4

US-10-062-109A-328  
; Sequence 328, Application US/10062109A  
; Publication No. US20030165505A1  
; GENERAL INFORMATION:  
; APPLICANT: Agensys  
; APPLICANT: Challita-Eid, Pia M.  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Farris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of  
; FILE REFERENCE: 51158-20062.01  
; CURRENT APPLICATION NUMBER: US/10/062,109A  
; CURRENT FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: US 10/005,480  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 765  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 328  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-062-109A-328

Query Match 58.0%; Score 29; DB 14; Length 10;  
Best Local Similarity 62.5%; Pred. No. 93;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPDENFK 8  
| | | | |  
Db 3 RKPDQHF 10

## RESULT 5

US-10-005-480A-328  
; Sequence 328, Application US/10005480A  
; Publication No. US20030191073A1  
; GENERAL INFORMATION:  
; APPLICANT: Agensys  
; APPLICANT: Challita-Eid, Pia M.  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Farris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of  
; FILE REFERENCE: 51158-20062.00  
; CURRENT APPLICATION NUMBER: US/10/005,480A  
; CURRENT FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 765  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 328  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-005-480A-328

Query Match 58.0%; Score 29; DB 14; Length 10;  
Best Local Similarity 62.5%; Pred. No. 93;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPDENFK 8  
| | | | |  
Db 3 RKPDQHF 10

## RESULT 6

US-09-880-748-2437



```
; Sequence 2437, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2437
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2437
```

```
Query Match          58.0%; Score 29; DB 10; Length 14;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 FPDENFKL 9
    |||:|
Db 7 FPGESFSL 14
```

```
RESULT 7
US-09-880-748-2684
; Sequence 2684, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2684
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2684
```

```
Query Match          58.0%; Score 29; DB 10; Length 14;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 FPDENFKL 9
    |||:|
Db 7 FPDHSEFL 14
```

RESULT 8

```
US-10-293-418-2437
; Sequence 2437, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2437
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2437
```

```
Query Match          58.0%; Score 29; DB 12; Length 14;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 FPDENFKL 9
    |||:|
Db 7 FPGESFSL 14
```

```
RESULT 9
US-10-293-418-2684
; Sequence 2684, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2684
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2684
```

```
QY 2 FPDENFKL 9
    |||:|
Db 7 FPDHSEFL 14
```

Query Match 58.0%; Score 29; DB 12; Length 14;  
Best Local Similarity 62.5%; Pred. No. 1.3e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RPPDENFKL 9  
DB 7 PPDHSHFDL 14

## RESULT 10

US-10-226-629A-464  
; Sequence 464, Application US/10226629A  
; Publication No. US20030166504A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection  
; FILE REFERENCE: 5006.01  
; CURRENT APPLICATION NUMBER: US/10/226,629A  
; CURRENT FILING DATE: 2002-08-22  
; PRIOR APPLICATION NUMBER: US 60/314,182  
; PRIOR FILING DATE: 2001-08-22  
; NUMBER OF SEQ ID NOS: 736  
; SOFTWARE: Patent version 3.1  
; SEQ ID NO 464  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Variola virus  
US-10-226-629A-464

Query Match 54.0%; Score 27; DB 14; Length 8;  
Best Local Similarity 57.1%; Pred. No. 1.2e+06;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPPDENF 7  
DB 1 KYPDLNF 7

## RESULT 11

US-10-226-629A-477  
; Sequence 477, Application US/10226629A  
; Publication No. US20030166504A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection  
; FILE REFERENCE: 5006.01  
; CURRENT APPLICATION NUMBER: US/10/226,629A  
; CURRENT FILING DATE: 2002-08-22  
; PRIOR APPLICATION NUMBER: US 60/314,182  
; PRIOR FILING DATE: 2001-08-22  
; NUMBER OF SEQ ID NOS: 736  
; SOFTWARE: Patent version 3.1  
; SEQ ID NO 477  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Variola virus  
US-10-226-629A-477

Query Match 54.0%; Score 27; DB 14; Length 8;  
Best Local Similarity 57.1%; Pred. No. 1.2e+06;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPPDENF 7  
DB 2 KYPDLNF 8

RESULT 12  
US-09-938-864-36  
; Sequence 36, Application US/09938864  
; Publication No. US20030072767A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Smithgall, Molly  
; APPLICANT: Moulton, Gus  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Sleath, Paul R.  
; APPLICANT: Mossman, Sally  
; APPLICANT: Evans, Lawrence  
; APPLICANT: Spies, A. Gregory  
; APPLICANT: Boydston, Jeremy  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI  
; FILE REFERENCE: 210121.465C5  
; CURRENT APPLICATION NUMBER: US/09/938,864  
; CURRENT FILING DATE: 2001-08-24  
; NUMBER OF SEQ ID NOS: 413  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 36  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-938-864-36

Query Match 54.0%; Score 27; DB 10; Length 9;  
Best Local Similarity 50.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPPDENFX 8  
DB 2 QFPNHSFX 9

## RESULT 13

US-09-791-477-36  
; Sequence 36, Application US/09791477  
; Publication No. US20030082194A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Cheever, Martin A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS  
; FILE REFERENCE: 2077.000200  
; CURRENT APPLICATION NUMBER: US/09/791,477  
; CURRENT FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: 60/184,070  
; PRIOR FILING DATE: 2000-02-22  
; NUMBER OF SEQ ID NOS: 326  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 36  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-791-477-36

Query Match 54.0%; Score 27; DB 10; Length 9;  
Best Local Similarity 50.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPPDENFX 8  
DB 2 QFPNHSFX 9

## RESULT 14

US-09-785-019-36  
; Sequence 36, Application US/09785019  
; Publication No. US20030082196A1

```
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Cheever, Martin A.
APPLICANT: McNeill, Patricia D.
APPLICANT: Smithgall, Molly
APPLICANT: Moulton, Gus
APPLICANT: Vedvick, Thomas S.
APPLICANT: Sleath, Paul
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
FILE REFERENCE: 210121.465C4
CURRENT APPLICATION NUMBER: US/09/785,019
CURRENT FILING DATE: 2001-02-15
NUMBER OF SEQ ID NOS: 376
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 36
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapien
US-09-785-019-36
```

```
Query Match          54.0%; Score 27; DB 10; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 RFPDENFK 8
   |||: |||
Db 2 QFPNHSFK 9
```

```
RESULT 15
US-10-125-635A-36
Sequence 36, Application US/10125635A
Publication No. US20030039635A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Smithgall, Molly D.
APPLICANT: Carter, Darick
APPLICANT: Cheever, Martin A.
APPLICANT: McNeill, Patricia D.
APPLICANT: Sutherland, R. Alec
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
FILE REFERENCE: 210121.465C7
CURRENT APPLICATION NUMBER: US/10/125,635A
CURRENT FILING DATE: 2002-07-19
NUMBER OF SEQ ID NOS: 461
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 36
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapien
US-10-125-635A-36
```

```
Query Match          54.0%; Score 27; DB 14; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 RFPDENFK 8
   |||: |||
Db 2 QFPNHSFK 9
```

```
RESULT 16
US-10-002-603-36
Sequence 36, Application US/10002603
Publication No. US20030095971A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: McNeill, Patricia D.
APPLICANT: Smithgall, Molly
APPLICANT: Moulton, Gus
APPLICANT: Vedvick, Thomas S.
```

```
APPLICANT: Sleath, Paul R.
APPLICANT: Mossman, Sally
APPLICANT: Evans, Lawrence
APPLICANT: Spies, A. Gregory
APPLICANT: Boydston, Jeremy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
FILE REFERENCE: 210121.465C6
CURRENT APPLICATION NUMBER: US/10/002,603
CURRENT FILING DATE: 2001-10-30
NUMBER OF SEQ ID NOS: 413
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 36
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapien
US-10-002-603-36
```

```
Query Match          54.0%; Score 27; DB 14; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 RFPDENFK 8
   |||: |||
Db 2 QFPNHSFK 9
```

```
RESULT 17
US-10-062-109A-7
Sequence 7, Application US/10062109A
Publication No. US20030165505A1
GENERAL INFORMATION:
APPLICANT: Agensys
APPLICANT: Challita-Eld, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Karen Jane Meyrick
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
FILE REFERENCE: 51158-20062.01
CURRENT APPLICATION NUMBER: US/10/062,109A
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: US 10/005,480
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 765
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-10-062-109A-7
```

```
Query Match          54.0%; Score 27; DB 14; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 3 PDENFK 8
   |||: |||
Db 2 PDQHF 7
```

```
RESULT 18
US-10-062-109A-560
Sequence 560, Application US/10062109A
Publication No. US20030165505A1
GENERAL INFORMATION:
APPLICANT: Agensys
APPLICANT: Challita-Eld, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Farris, Mary
```

```
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2108 Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 560
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-560
```

```
Query Match          54.0%; Score 27; DB 14; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 3 PDENFK 8
    ||:|
Db 2 PDQHK 7
```

```
RESULT 19
US-10-226-629A-465
; Sequence 465, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 465
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-465
```

```
Query Match          54.0%; Score 27; DB 14; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 RPDENF 7
    :|||
Db 1 KYPLNLF 7
```

```
RESULT 20
US-10-226-629A-478
; Sequence 478, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
```

```
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 478
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-478
```

```
Query Match          54.0%; Score 27; DB 14; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 RPDENF 7
    :|||
Db 2 KYPLNLF 8
```

```
RESULT 21
US-10-226-629A-491
; Sequence 491, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 491
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-491
```

```
Query Match          54.0%; Score 27; DB 14; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 RPDENF 7
    :|||
Db 3 KYPLNLF 9
```

```
RESULT 22
US-10-005-480A-7
; Sequence 7, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Ageneys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Farris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2108 Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 9
```

Thu Sep 2 07:41:42 2004

us-09-720-469a-7.aug30.rapb

Page 7

TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-005-480A-7

Query Match 54.0%; Score 27; DB 14; Length 9;  
Best Local Similarity 66.7%; Pred. No. 1.2e+06;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDENFK 8  
DB 2 PDQHF 7

RESULT 23  
US-10-005-480A-560  
Sequence 560, Application US/10005480A  
Publication No. US20030191073A1  
GENERAL INFORMATION:  
APPLICANT: Agensys  
APPLICANT: Challita-Eid, Pia M.  
APPLICANT: Raitano, Arthur B.  
APPLICANT: Paris, Mary  
APPLICANT: Hubert, Rene S.  
APPLICANT: Morrison, Karen Jane Meyrick  
APPLICANT: Jakobovits, Aya  
TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of  
TITLE OF INVENTION: Cancer  
FILE REFERENCE: 51158-20062.00  
CURRENT APPLICATION NUMBER: US/10/005,480A  
CURRENT FILING DATE: 2001-11-07  
NUMBER OF SEQ ID NOS: 765  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 560  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-005-480A-560

Query Match 54.0%; Score 27; DB 14; Length 9;  
Best Local Similarity 66.7%; Pred. No. 1.2e+06;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDENFK 8  
DB 2 PDQHF 7

RESULT 24  
US-10-195-835-36  
Sequence 36, Application US/10195835  
Publication No. US20030198222A1  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: Smithgall, Molly D.  
APPLICANT: Carter, Darick  
APPLICANT: Cheever, Martin A.  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Sutherland, R. Alec  
APPLICANT: Mossman, Sally P.  
APPLICANT: Evans, Lawrence S.  
APPLICANT: Swanson, Ryan M.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY  
FILE REFERENCE: 210121.465C8  
CURRENT APPLICATION NUMBER: US/10/195,835,  
CURRENT FILING DATE: 2002-07-12  
NUMBER OF SEQ ID NOS: 461  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 36  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapien

US-10-195-835-36

Query Match 54.0%; Score 27; DB 14; Length 9;  
Best Local Similarity 50.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RFPDENFK 8  
DB 2 QFPNHSFK 9

RESULT 25  
US-10-286-333-36  
Sequence 36, Application US/10286333  
Publication No. US20030215458A1  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Jaya, No. US20030215458A1a1e  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY  
FILE REFERENCE: 210121.465C10  
CURRENT APPLICATION NUMBER: US/10/286,333  
CURRENT FILING DATE: 2002-10-30  
NUMBER OF SEQ ID NOS: 506  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 36  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapien  
US-10-286-333-36

Query Match 54.0%; Score 27; DB 15; Length 9;  
Best Local Similarity 50.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RFPDENFK 8  
DB 2 QFPNHSFK 9

RESULT 26  
US-10-244-830-36  
Sequence 36, Application US/10244830  
Publication No. US2003023557A1  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: Cheever, Martin A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY  
FILE REFERENCE: 210121.465C9  
CURRENT APPLICATION NUMBER: US/10/244,830  
CURRENT FILING DATE: 2002-09-16  
NUMBER OF SEQ ID NOS: 468  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 36  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapien  
US-10-244-830-36

Query Match 54.0%; Score 27; DB 15; Length 9;  
Best Local Similarity 50.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RFPDENFK 8  
DB 2 QFPNHSFK 9

RESULT 27  
US-10-427-717-36  
Sequence 36, Application US/10427717

```

; Publication No. US20040018204A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Jaya, No. US20040018204A1a1a1e
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C11
; CURRENT APPLICATION NUMBER: US/10/427,717
; PRIORITY FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 508
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
; US-10-427-717-36

```

```

Query Match      54.0%; Score 27; DB 15; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 RPPDENFX 8
        ||:|
Db      2 QFPNHSFX 9

```

```

RESULT 28
US-10-648-780-36
; Sequence 36, Application US/10648780
; Publication No. US20040126362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Smithgall, Molly D.
; APPLICANT: Carter, Patrick
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sutherland, R. Alec
; APPLICANT: Mossman, Sally P.
; APPLICANT: Evans, Lawrence S.
; APPLICANT: Swanson, Ryan M.
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C8
; CURRENT APPLICATION NUMBER: US/10/648,780
; PRIORITY FILING DATE: 2003-08-26
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
; US-10-648-780-36

```

```

Query Match      54.0%; Score 27; DB 16; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 RPPDENFX 8
        ||:|
Db      2 QFPNHSFX 9

```

```

RESULT 29
US-10-062-109A-196
; Sequence 196, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Chailita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.

```

```

; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; PRIORITY FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 196
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-062-109A-196

```

```

Query Match      54.0%; Score 27; DB 14; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      3 PDENFX 8
        ||:|
Db      2 PDQHF 7

```

```

RESULT 30
US-10-062-109A-427
; Sequence 427, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Chailita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; PRIORITY FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 427
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-062-109A-427

```

```

Query Match      54.0%; Score 27; DB 14; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      3 PDENFX 8
        ||:|
Db      2 PDQHF 7

```

```

RESULT 31
US-10-062-109A-507
; Sequence 507, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Chailita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary

```

```
APPLICANT: Hubert, Rene S.
APPLICANT: Moritzson, Karen Jane Meyrick
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
TITLE OF INVENTION: Cancer
FILE REFERENCE: 51158-20062.01
CURRENT APPLICATION NUMBER: US/10/062,109A
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: US 10/005,480
NUMBER OF SEQ ID NOS: 765
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 507
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-10-062-109A-507
```

```
Query Match          54.0%; Score 27; DB 14; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 3 PDENFK 8
Db 2 PDQHF 7
```

```
RESULT 32
US-10-062-109A-614
Sequence 614, Application US/10062109A
Publication No. US20030165505A1
GENERAL INFORMATION:
APPLICANT: Agensys
APPLICANT: Challita-Eld, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Paris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Moritzson, Karen Jane Meyrick
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
TITLE OF INVENTION: Cancer
FILE REFERENCE: 51158-20062.01
CURRENT APPLICATION NUMBER: US/10/062,109A
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: US 10/005,480
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 765
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 614
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-10-062-109A-614
```

```
Query Match          54.0%; Score 27; DB 14; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 3 PDENFK 8
Db 2 PDQHF 7
```

```
RESULT 33
US-10-226-629A-466
Sequence 466, Application US/10226629A
Publication No. US20030165504A1
GENERAL INFORMATION:
APPLICANT: Myriad Genetics, Inc.
APPLICANT: Morham, Scott
APPLICANT: Zavitz, Kenton
```

```
APPLICANT: Hobden, Adrian
TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
FILE REFERENCE: 5006.01
CURRENT APPLICATION NUMBER: US/10/226,629A
CURRENT FILING DATE: 2002-08-22
PRIOR APPLICATION NUMBER: US 60/314,182
PRIOR FILING DATE: 2001-08-22
NUMBER OF SEQ ID NOS: 736
SOFTWARE: PatentIn version 3.1
SEQ ID NO 466
LENGTH: 10
TYPE: PRT
ORGANISM: Variola virus
US-10-226-629A-466
```

```
Query Match          54.0%; Score 27; DB 14; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 RPPDENF 7
Db 1 KYFDLNF 7
```

```
RESULT 34
US-10-226-629A-479
Sequence 479, Application US/10226629A
Publication No. US20030165504A1
GENERAL INFORMATION:
APPLICANT: Myriad Genetics, Inc.
APPLICANT: Morham, Scott
APPLICANT: Zavitz, Kenton
APPLICANT: Hobden, Adrian
TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
FILE REFERENCE: 5006.01
CURRENT APPLICATION NUMBER: US/10/226,629A
CURRENT FILING DATE: 2002-08-22
PRIOR APPLICATION NUMBER: US 60/314,182
PRIOR FILING DATE: 2001-08-22
NUMBER OF SEQ ID NOS: 736
SOFTWARE: PatentIn version 3.1
SEQ ID NO 479
LENGTH: 10
TYPE: PRT
ORGANISM: Variola virus
US-10-226-629A-479
```

```
Query Match          54.0%; Score 27; DB 14; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 RPPDENF 7
Db 2 KYFDLNF 8
```

```
RESULT 35
US-10-226-629A-492
Sequence 492, Application US/10226629A
Publication No. US20030165504A1
GENERAL INFORMATION:
APPLICANT: Myriad Genetics, Inc.
APPLICANT: Morham, Scott
APPLICANT: Zavitz, Kenton
APPLICANT: Hobden, Adrian
TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
FILE REFERENCE: 5006.01
CURRENT APPLICATION NUMBER: US/10/226,629A
CURRENT FILING DATE: 2002-08-22
PRIOR APPLICATION NUMBER: US 60/314,182
PRIOR FILING DATE: 2001-08-22
NUMBER OF SEQ ID NOS: 736
SOFTWARE: PatentIn version 3.1
```

SEQ ID NO 492  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Variola virus  
US-10-226-629A-492

Query Match  
Best Local Similarity 54.0%; Score 27; DB 14; Length 10;  
Best Local Similarity 57.1%; Pred. No. 2.2e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPPDENF 7  
Db 3 KYPDLNF 9

RESULT 36  
US-10-226-629A-505  
Sequence 505, Application US/10226629A  
Publication No. US20030191073A1  
GENERAL INFORMATION:  
APPLICANT: Myriad Genetics, Inc.  
APPLICANT: Morham, Scott  
APPLICANT: Zavit, Kenton  
APPLICANT: Hobden, Adrian  
TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection  
FILE REFERENCE: 5006.01  
CURRENT APPLICATION NUMBER: US/10/226,629A  
CURRENT FILING DATE: 2002-08-22  
PRIOR APPLICATION NUMBER: US 60/314,182  
PRIOR FILING DATE: 2001-08-22  
NUMBER OF SEQ ID NOS: 736  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 505  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Variola virus  
US-10-226-629A-505

Query Match  
Best Local Similarity 54.0%; Score 27; DB 14; Length 10;  
Best Local Similarity 57.1%; Pred. No. 2.2e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPPDENF 7  
Db 4 KYPDLNF 10

RESULT 37  
US-10-005-480A-196  
Sequence 196, Application US/10005480A  
Publication No. US20030191073A1  
GENERAL INFORMATION:  
APPLICANT: Agensys  
APPLICANT: Chailita-Eid, Pia M.  
APPLICANT: Raitano, Arthur B.  
APPLICANT: Paris, Mary  
APPLICANT: Hubert, Rene S.  
APPLICANT: Morrison, Karen Jane Meyrick  
TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of  
FILE REFERENCE: 51158-20062.00  
CURRENT APPLICATION NUMBER: US/10/005,480A  
CURRENT FILING DATE: 2001-11-07  
NUMBER OF SEQ ID NOS: 765  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 196  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-005-480A-196

Query Match  
Best Local Similarity 54.0%; Score 27; DB 14; Length 10;  
Best Local Similarity 66.7%; Pred. No. 2.2e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDENFX 8  
Db 2 PDQHXF 7

RESULT 38  
US-10-005-480A-427  
Sequence 427, Application US/10005480A  
Publication No. US20030191073A1  
GENERAL INFORMATION:  
APPLICANT: Agensys  
APPLICANT: Chailita-Eid, Pia M.  
APPLICANT: Raitano, Arthur B.  
APPLICANT: Paris, Mary  
APPLICANT: Hubert, Rene S.  
APPLICANT: Morrison, Karen Jane Meyrick  
TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of  
FILE REFERENCE: 51158-20062.00  
CURRENT APPLICATION NUMBER: US/10/005,480A  
CURRENT FILING DATE: 2001-11-07  
NUMBER OF SEQ ID NOS: 765  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 427  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-005-480A-427

Query Match  
Best Local Similarity 54.0%; Score 27; DB 14; Length 10;  
Best Local Similarity 66.7%; Pred. No. 2.2e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDENFX 8  
Db 2 PDQHXF 7

RESULT 39  
US-10-005-480A-507  
Sequence 507, Application US/10005480A  
Publication No. US20030191073A1  
GENERAL INFORMATION:  
APPLICANT: Agensys  
APPLICANT: Chailita-Eid, Pia M.  
APPLICANT: Raitano, Arthur B.  
APPLICANT: Paris, Mary  
APPLICANT: Hubert, Rene S.  
APPLICANT: Morrison, Karen Jane Meyrick  
TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of  
FILE REFERENCE: 51158-20062.00  
CURRENT APPLICATION NUMBER: US/10/005,480A  
CURRENT FILING DATE: 2001-11-07  
NUMBER OF SEQ ID NOS: 765  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 507  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-005-480A-507

Query Match  
Best Local Similarity 54.0%; Score 27; DB 14; Length 10;  
Best Local Similarity 66.7%; Pred. No. 2.2e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;



Thu Sep 2 07:41:42 2004

us-09-720-469a-7.aug30.rapb

Page 11

QY 3 PDENFK 8  
Db 2 PDQHK 7

RESULT 40

US-10-005-480A-614  
; Sequence 614, Application US/10005480A  
; Publication No. US20030191072A1  
; GENERAL INFORMATION:  
; APPLICANT: Agensys  
; APPLICANT: Chailita-Bid, Pia M.  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of  
; FILE REFERENCE: 51158-20062.00  
; CURRENT APPLICATION NUMBER: US/10/005.480A  
; CURRENT FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 765  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 614  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-005-480A-614

Query Match 54.0%; Score 27; DB 14; Length 10;  
Best Local Similarity 66.7%; Pred. No. 2.2e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDENFK 8  
Db 2 PDQHK 7

RESULT 41  
US-10-226-629A-467  
; Sequence 467, Application US/10226629A  
; Publication No. US20030166504A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavit, Kenton  
; APPLICANT: Zavit, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection  
; FILE REFERENCE: 5006.01  
; CURRENT APPLICATION NUMBER: US/10/226.629A  
; CURRENT FILING DATE: 2002-08-22  
; PRIOR APPLICATION NUMBER: US 60/314,182  
; PRIOR FILING DATE: 2001-08-22  
; NUMBER OF SEQ ID NOS: 736  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 467  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Variola virus  
US-10-226-629A-467

Query Match 54.0%; Score 27; DB 14; Length 11;  
Best Local Similarity 57.1%; Pred. No. 2.4e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPPDENF 7  
Db 3 KYPDINF 9

RESULT 42  
US-10-226-629A-480  
; Sequence 480, Application US/10226629A  
; Publication No. US20030166504A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavit, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection  
; FILE REFERENCE: 5006.01  
; CURRENT APPLICATION NUMBER: US/10/226.629A  
; CURRENT FILING DATE: 2002-08-22  
; PRIOR APPLICATION NUMBER: US 60/314,182  
; PRIOR FILING DATE: 2001-08-22  
; NUMBER OF SEQ ID NOS: 736  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 480  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Variola virus  
US-10-226-629A-480

Query Match 54.0%; Score 27; DB 14; Length 11;  
Best Local Similarity 57.1%; Pred. No. 2.4e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPPDENF 7  
Db 3 KYPDINF 9

RESULT 43  
US-10-226-629A-493  
; Sequence 493, Application US/10226629A  
; Publication No. US20030166504A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavit, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection  
; FILE REFERENCE: 5006.01  
; CURRENT APPLICATION NUMBER: US/10/226.629A  
; CURRENT FILING DATE: 2002-08-22  
; PRIOR APPLICATION NUMBER: US 60/314,182  
; PRIOR FILING DATE: 2001-08-22  
; NUMBER OF SEQ ID NOS: 736  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 493  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Variola virus  
US-10-226-629A-493

Query Match 54.0%; Score 27; DB 14; Length 11;  
Best Local Similarity 57.1%; Pred. No. 2.4e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPPDENF 7  
Db 3 KYPDINF 9

RESULT 44  
US-10-226-629A-506  
; Sequence 506, Application US/10226629A  
; Publication No. US20030166504A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavit, Kenton  
; APPLICANT: Hobden, Adrian

;; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection  
;; FILE REFERENCE: 5006.01  
;; CURRENT APPLICATION NUMBER: US/10/226,629A  
;; CURRENT FILING DATE: 2002-08-22  
;; PRIOR APPLICATION NUMBER: US 60/314,182  
;; PRIOR FILING DATE: 2001-08-22  
;; NUMBER OF SEQ ID NOS: 736  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 506  
;; LENGTH: 11  
;; TYPE: PRT  
;; ORGANISM: Variola virus  
US-10-226-629A-506

Query Match 54.0%; Score 27; DB 14; Length 11;  
Best Local Similarity 57.1%; Pred. No. 2.4e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPPDENF 7  
::|||  
Db 4 KYPDLNF 10

RESULT 45  
US-10-226-629A-518  
;; Sequence 518, Application US/10226629A  
;; Publication No. US20030166504A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Myriad Genetics, Inc.  
;; APPLICANT: Morham, Scott  
;; APPLICANT: Zavit, Kenton  
;; APPLICANT: Hobden, Adrian  
;; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection  
;; FILE REFERENCE: 5006.01  
;; CURRENT APPLICATION NUMBER: US/10/226,629A  
;; CURRENT FILING DATE: 2002-08-22  
;; PRIOR APPLICATION NUMBER: US 60/314,182  
;; PRIOR FILING DATE: 2001-08-22  
;; NUMBER OF SEQ ID NOS: 736  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 518  
;; LENGTH: 11  
;; TYPE: PRT  
;; ORGANISM: Variola virus  
US-10-226-629A-518

Query Match 54.0%; Score 27; DB 14; Length 11;  
Best Local Similarity 57.1%; Pred. No. 2.4e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPPDENF 7  
::|||  
Db 5 KYPDLNF 11

Search completed: August 30, 2004, 11:04:59  
Job time : 12.0066 secs

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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:59 ; Search time 3.55743 Seconds  
(without alignments)  
130.609 Million cell updates/sec

Title: US-09-720-469A-7  
Perfect score: 50  
Sequence: 1 RFPDENFKL 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 78885

Minimum DB seq length: 8  
Maximum DB seq length: 14

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA: \*  
1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep: \*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep: \*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep: \*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep: \*  
5: /cgn2\_6/ptodata/2/1aa/PTUTS.COMB.pep: \*  
6: /cgn2\_6/ptodata/2/1aa/backfile1.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	62.0	10	2	US-08-658-639-8
2	31	62.0	10	3	US-08-944-604-8
3	29	58.0	10	5	PCR-US93-08067-4
4	28	56.0	14	3	US-09-041-886-48
5	25	50.0	10	1	US-08-290-448A-2
6	25	50.0	10	1	US-08-290-448A-2
7	25	50.0	10	1	US-08-175-068A-2
8	25	50.0	10	4	US-08-461-938B-2
9	25	50.0	10	4	US-08-461-938B-2
10	25	50.0	11	4	US-08-290-448A-34
11	25	50.0	11	1	US-08-290-448A-34
12	25	50.0	11	1	US-08-175-068A-34
13	25	50.0	11	4	US-08-461-938B-34
14	25	50.0	11	4	US-08-461-938B-34
15	24	48.0	8	1	US-08-378-853-3
16	24	48.0	8	3	US-08-970-648-3
17	24	48.0	8	4	US-08-952-558-4
18	24	48.0	9	2	US-08-522-269B-6
19	24	48.0	9	2	US-09-294-923-6
20	24	48.0	9	3	US-08-960-780-59
21	24	48.0	9	3	US-09-073-898-59
22	24	48.0	9	4	US-09-341-982-21
23	24	48.0	9	4	US-09-850-351A-59
24	24	48.0	10	4	US-09-341-982-36
25	24	48.0	11	4	US-09-341-982-58
26	24	48.0	12	4	US-08-934-223-25
27	24	48.0	12	2	US-08-933-403-25

28	24	48.0	12	2	US-09-207-621-25	Sequence 25, Appl
29	24	48.0	12	2	US-08-532-818-25	Sequence 25, Appl
30	24	48.0	12	3	US-09-231-797-25	Sequence 25, Appl
31	24	48.0	12	3	US-08-934-224-25	Sequence 25, Appl
32	24	48.0	12	3	US-08-933-843-25	Sequence 25, Appl
33	24	48.0	12	3	US-08-934-223-25	Sequence 25, Appl
34	24	48.0	12	3	US-09-413-492-25	Sequence 25, Appl
35	23	46.0	9	1	US-08-615-181-91	Sequence 25, Appl
36	23	46.0	9	4	US-09-492-543-73	Sequence 73, Appl
37	23	46.0	9	4	US-09-492-543-101	Sequence 101, Appl
38	23	46.0	9	4	US-09-688-188B-113	Sequence 113, Appl
39	23	46.0	10	1	US-09-291-417D-113	Sequence 113, Appl
40	23	46.0	10	1	US-08-261-206A-110	Sequence 110, Appl
41	23	46.0	10	1	US-08-261-206A-31	Sequence 31, Appl
42	23	46.0	10	1	US-08-261-206A-35	Sequence 35, Appl
43	23	46.0	10	1	US-08-261-206A-39	Sequence 39, Appl
44	23	46.0	10	1	US-08-261-206A-43	Sequence 43, Appl
45	23	46.0	10	4	US-09-688-188B-79	Sequence 79, Appl

## ALIGNMENTS

RESULT 1  
US-08-658-639-8  
Sequence 8, Application US/08658639  
Patent No. 5914238  
GENERAL INFORMATION:  
APPLICANT: KESSEE, SUSAN  
APPLICANT: OBAR, ROBERT  
TITLE OF INVENTION: WU, YING-JYE  
TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Testa, Hurwitz & Thibault  
STREET: 125 High St.  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/658,639  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: MEYERS, THOMAS C  
REGISTRATION NUMBER: 36,989  
REFERENCE/DOCKET NUMBER: MTP-021 (8395/24)  
TELEPHONE: (617) 248-7100  
TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-658-639-8  
Query Match 62.0%; Score 31; DB 2; Length 10;  
Best Local Similarity 66.7%; Pred. No. 8.4;  
Matches 6; Conservative 1; Mismatches 0; Gaps 0;  
QY 1 RFPDENFKL 9  
Db 1 KFPDENFKL 9

RESULT 2  
US-08-944-604-8  
Sequence 8, Application US/08944604  
Patent No. 6218131  
GENERAL INFORMATION:  
APPLICANT: KESSEE, SUSAN  
APPLICANT: OBAR, ROBERT  
APPLICANT: WU, YING-JYE  
TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF  
TITLE OF INVENTION: BREAST CANCER  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Testa, Hurwitz & Thibault  
STREET: 125 High St.  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/944,604  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MEYERS, THOMAS C  
REGISTRATION NUMBER: 36,989  
REFERENCE/DOCKET NUMBER: MTP-021 (8395/24)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-944-604-8

Query Match 62.0%; Score 31; DB 3; Length 10;  
Best Local Similarity 66.7%; Pred. No. 8.4;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RFPDENFK 9  
DB 1 KFDDENFIL 9

RESULT 3  
PCT-US93-08067-4  
Sequence 4, Application PC/TUS9308067  
GENERAL INFORMATION:  
APPLICANT: Silva, Robert F  
APPLICANT: Reilly, John D  
TITLE OF INVENTION: PORTABLE INTRON AS AN INSERTION VECTOR FOR  
TITLE OF INVENTION: GENE INSERTION  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jacobson, Price, Holman & Steern  
STREET: 400 Seventh St. N.W.  
CITY: Washington D.C.  
COUNTRY: U.S.A.  
ZIP: 20004-2201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/08067  
FILING DATE: 27-AUG-1993  
CLASSIFICATION:  
CLASSIFICATION: 435/235  
CLASSIFICATION: C12N 7/00  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. Application No. 07/936,423  
FILING DATE: 27-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Holman, John C.  
REGISTRATION NUMBER: 22,769  
REFERENCE/DOCKET NUMBER: Q43813PC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 638-6666  
TELEFAX: (202) 393-5350  
TELEX: RCA 248593 IDEA UR  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US93-08067-4

Query Match 58.0%; Score 29; DB 5; Length 10;  
Best Local Similarity 57.1%; Pred. No. 20;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PFDENFK 8  
DB 4 YPDNFK 10

RESULT 4  
US-09-041-886-48  
Sequence 48, Application US/09041886  
Patent No. 6235872  
GENERAL INFORMATION:  
APPLICANT: Bredesen, Dale E.  
APPLICANT: Rabinzaden, Shartoz  
TITLE OF INVENTION: Proapoptotic Peptides, Dependence  
TITLE OF INVENTION: Polypeptides and Methods of Use  
NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell & Flores LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/041,886  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LJ 2626  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 48:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

MOLECULE TYPE: peptide  
US-09-041-886-48

Query Match 56.0%; Score 28; DB 3; Length 14;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DENFX 8  
| | | | |  
Db 2 DENFX 6

RESULT 5  
US-08-290-448A-2  
Sequence 2, Application US/08290448A  
Patent No. 5676954  
GENERAL INFORMATION:  
APPLICANT: Rogers, Bruce  
APPLICANT: Klapper, David G.  
APPLICANT: Rafnar, Thorunn  
APPLICANT: Kuo, Mei-chang  
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses  
NUMBER OF SEQUENCES: 93  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/290,448A  
FILING DATE: August 15, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/529,951  
FILING DATE: May 29, 1990  
APPLICATION NUMBER: US 07/325,365  
FILING DATE: March 17, 1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Amy E. Mandragouras  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: IMI-018CN  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-5941  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-290-448A-2

Query Match 50.0%; Score 25; DB 1; Length 10;  
Best Local Similarity 83.3%; Pred. No. 1,1e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PDENFX 8  
| | | | |  
Db 5 PDENFX 10

RESULT 6  
US-08-290-448A-2  
Sequence 2, Application US/08290448A  
Patent No. 5688204  
GENERAL INFORMATION:

APPLICANT: Rogers, Bruce  
APPLICANT: Klapper, David G.  
APPLICANT: Rafnar, Thorunn  
APPLICANT: Kuo, Mei-chang  
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses  
NUMBER OF SEQUENCES: 93  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/290,448A  
FILING DATE: August 15, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/529,951  
FILING DATE: May 29, 1990  
APPLICATION NUMBER: US 07/325,365  
FILING DATE: March 17, 1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Amy E. Mandragouras  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: IMI-018CN  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-290-448A-2

Query Match 50.0%; Score 25; DB 1; Length 10;  
Best Local Similarity 83.3%; Pred. No. 1,1e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PDENFX 8  
| | | | |  
Db 5 PDENFX 10

RESULT 7  
US-08-175-069A-2  
Sequence 2, Application US/08175069A  
Patent No. 5776761  
GENERAL INFORMATION:  
APPLICANT: Rogers, Bruce  
APPLICANT: Klapper, David G.  
APPLICANT: Rafnar, Thorunn  
APPLICANT: Kuo, Mei-chang  
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses  
NUMBER OF SEQUENCES: 93  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/175,069A  
FILING DATE: December 29, 1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/529,951  
FILING DATE: May 29, 1990  
APPLICATION NUMBER: US 07/325,365  
FILING DATE: March 17, 1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Amy E. Mandragouras  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: IMI-018DV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-175-069A-2

Query Match 50.0%; Score 25; DB 1; Length 10;  
Best Local Similarity 83.3%; Pred. No. 1.1e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PDENFK 8  
| | | | |  
Db 5 PWENFK 10

RESULT 8  
US-08-461-939B-2  
Sequence 2, Application US/08461939B  
Patent No. 6335019  
GENERAL INFORMATION:  
APPLICANT: Rogers, Bruce  
APPLICANT: Klapper, David G.  
APPLICANT: Ratnar, Thorunn  
APPLICANT: Kuo, Mei-chang  
TITLE OF INVENTION: Methods For Treating Sensitivity To A  
NUMBER OF SEQUENCES: 93  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,939B  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/464,000  
FILING DATE: 05-JUN-1995  
APPLICATION NUMBER: US 08/290,448  
FILING DATE: 15-AUG-1994  
APPLICATION NUMBER: US 07/529,951  
FILING DATE: 29-MAY-1990  
APPLICATION NUMBER: US 07/325,365  
FILING DATE: 17-MAR-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Amy E. Mandragouras  
REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: IMI-018CNDV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-461-939B-2

Query Match 50.0%; Score 25; DB 4; Length 10;  
Best Local Similarity 83.3%; Pred. No. 1.1e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PDENFK 8  
| | | | |  
Db 5 PWENFK 10

RESULT 9  
US-08-464-000-2  
Sequence 2, Application US/08464000  
Patent No. 6335020  
GENERAL INFORMATION:  
APPLICANT: Rogers, Bruce  
APPLICANT: Klapper, David G.  
APPLICANT: Ratnar, Thorunn  
APPLICANT: Kuo, Mei-chang  
TITLE OF INVENTION: Allergenic Peptides from Ragweed Pollen  
NUMBER OF SEQUENCES: 93  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/464,000  
FILING DATE: 05-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/290,448  
FILING DATE: 15-AUG-1994  
APPLICATION NUMBER: US 07/529,951  
FILING DATE: 29-MAY-1990  
APPLICATION NUMBER: US 07/325,365  
FILING DATE: 17-MAR-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Amy E. Mandragouras  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: IMI-018CN2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-464-000-2

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PDENFK 8  
| | | | |

Db 5 PWENFK 10

RESULT 10

US-08-290-448A-34

; Sequence 34, Application US/08290448A

; Patent No. 5676954

; GENERAL INFORMATION:

; APPLICANT: Rogers, Bruce

; APPLICANT: Klapper, David G.

; APPLICANT: Rafnar, Thorunn

; APPLICANT: Kuo, Mei-chang

; TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses

; NUMBER OF SEQUENCES: 93

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 State Street, suite 510

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109-1875

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/290,448A

; FILING DATE: August 15, 1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/529,951

; FILING DATE: May 29, 1990

; APPLICATION NUMBER: US 07/325,365

; FILING DATE: March 17, 1989

; ATTORNEY/AGENT INFORMATION:

; NAME: Amy E. Mandagouras

; REGISTRATION NUMBER: 36,207

; REFERENCE/DOCKET NUMBER: IMI-018CN

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617)227-7400

; TELEFAX: (617)227-5941

; INFORMATION FOR SEQ ID NO: 34:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FRAGMENT TYPE: internal

US-08-290-448A-34

Query Match 50.0%; Score 25; DB 1; Length 11;

Best Local Similarity 83.3%; Pred. No. 1.2e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PDENFK 8  
| | | | |

Db 5 PWENFK 10

RESULT 11

US-08-290-448A-34

; Sequence 34, Application US/08290448A

; Patent No. 5676954

; GENERAL INFORMATION:

; APPLICANT: Rogers, Bruce

; APPLICANT: Klapper, David G.

; APPLICANT: Rafnar, Thorunn

; APPLICANT: Kuo, Mei-chang

; TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses

NUMBER OF SEQUENCES: 93

CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 State Street, suite 510

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109-1875

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/290,448A

; FILING DATE: August 15, 1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/529,951

; FILING DATE: May 29, 1990

; APPLICATION NUMBER: US 07/325,365

; FILING DATE: March 17, 1989

; ATTORNEY/AGENT INFORMATION:

; NAME: Amy E. Mandagouras

; REGISTRATION NUMBER: 36,207

; REFERENCE/DOCKET NUMBER: IMI-018CN

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617)227-7400

; TELEFAX: (617)227-5941

; INFORMATION FOR SEQ ID NO: 34:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FRAGMENT TYPE: internal

US-08-290-448A-34

Query Match 50.0%; Score 25; DB 1; Length 11;

Best Local Similarity 83.3%; Pred. No. 1.2e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PDENFK 8  
| | | | |

Db 5 PWENFK 10

RESULT 12

US-08-175-069A-34

; Sequence 34, Application US/08175069A

; Patent No. 5776761

; GENERAL INFORMATION:

; APPLICANT: Rogers, Bruce

; APPLICANT: Klapper, David G.

; APPLICANT: Rafnar, Thorunn

; APPLICANT: Kuo, Mei-chang

; TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses

; NUMBER OF SEQUENCES: 93

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD, LLP

; STREET: 60 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109-1875

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/175,069A

; FILING DATE: December 29, 1993

; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/529,951  
FILING DATE: May 29, 1990  
APPLICATION NUMBER: US 07/325,365  
FILING DATE: March 17, 1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Amy E. Mandragouras  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: IMI-018DV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-175-069A-34

Query Match 50.0%; Score 25; DB 1; Length 11;  
Best Local Similarity 83.3%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PDENFK 8  
Db 5 FWNENFK 10

RESULT 13  
US-08-461-939B-34  
Sequence 34, Application US/08461939B  
Patent No. 6335019  
GENERAL INFORMATION:  
APPLICANT: Rogers, Bruce  
APPLICANT: Klapper, David G.  
APPLICANT: Rafnar, Thorunn  
APPLICANT: Kuo, Mei-chang  
TITLE OF INVENTION: Methods For Treating Sensitivity To A  
TITLE OF INVENTION: Protein Allergen Using Peptides Which Include A T Cell Epitope  
NUMBER OF SEQUENCES: 93  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,939B  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/464,000  
FILING DATE: 05-JUN-1995  
APPLICATION NUMBER: US 08/290,448  
FILING DATE: 15-AUG-1994  
APPLICATION NUMBER: US 07/529,951  
FILING DATE: 29-MAY-1990  
APPLICATION NUMBER: US 07/325,365  
FILING DATE: 17-MAR-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Amy E. Mandragouras  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: IMI-018CNDV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-461-939B-34

Query Match 50.0%; Score 25; DB 4; Length 11;  
Best Local Similarity 83.3%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PDENFK 8  
Db 5 FWNENFK 10

RESULT 14  
US-08-464-000-34  
Sequence 34, Application US/08464000  
Patent No. 6335020  
GENERAL INFORMATION:  
APPLICANT: Rogers, Bruce  
APPLICANT: Klapper, David G.  
APPLICANT: Rafnar, Thorunn  
APPLICANT: Kuo, Mei-chang  
TITLE OF INVENTION: Allergenic Peptides from Ragweed Pollen  
NUMBER OF SEQUENCES: 93  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/464,000  
FILING DATE: 05-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/290,448  
FILING DATE: 15-AUG-1994  
APPLICATION NUMBER: US 07/529,951  
FILING DATE: 29-MAY-1990  
APPLICATION NUMBER: US 07/325,365  
FILING DATE: 17-MAR-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Amy E. Mandragouras  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: IMI-018CN2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-464-000-34

Query Match 50.0%; Score 25; DB 4; Length 11;  
Best Local Similarity 83.3%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PDENFK 8  
Db 5 FWNENFK 10



RESULT 15  
US-08-378-859-3  
Sequence 3, Application US/08378859  
Patent No. 5728553  
GENERAL INFORMATION:  
APPLICANT: Goodey, Andrew R  
APPLICANT: Sleep, Darrell  
APPLICANT: van Uik, Hendrik  
APPLICANT: Berzenko, Stephen  
APPLICANT: Woodrow, John R  
APPLICANT: Johnson, Richard A  
APPLICANT: Wood, Patricia C  
APPLICANT: Burton, Steven J  
APPLICANT: Quirk, Alan V  
TITLE OF INVENTION: High Purity Albumin  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: The BOC Group, Inc  
STREET: 100 Mountain Avenue  
CITY: Murray Hill, New Providence  
STATE: New Jersey  
COUNTRY: United States of America  
ZIP: 07974  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/378, 859  
FILING DATE: 26-JAN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Swode, R Hain  
REGISTRATION NUMBER: 24,864  
REFERENCE/DOCKET NUMBER: 92H8501  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 771 6292  
TELEFAX: (908) 771 6159  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Peptide fragment of human serum albumin  
US-08-378-859-3

Query Match 48.0%; Score 24; DB 1; Length 8;  
Best Local Similarity 80.0%; Pred. No. 3e+05; 0; Indels 0; Gaps 0;  
Matches 4; Conservative 1; Mismatches 0;

QY 4 DENFK 8  
:||||  
Db 4 EENFK 8

RESULT 16  
US-08-970-648-3  
Sequence 3, Application US/08970648  
Patent No. 6034221  
GENERAL INFORMATION:  
APPLICANT: Goodey, Andrew R  
APPLICANT: Sleep, Darrell  
APPLICANT: van Uik, Hendrik  
APPLICANT: Berzenko, Stephen

APPLICANT: Woodrow, John R  
APPLICANT: Johnson, Richard A  
APPLICANT: Wood, Patricia C  
APPLICANT: Burton, Steven J  
APPLICANT: Quirk, Alan V  
TITLE OF INVENTION: High Purity Albumin  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: The BOC Group, Inc  
STREET: 100 Mountain Avenue  
CITY: Murray Hill, New Providence  
STATE: New Jersey  
COUNTRY: United States of America  
ZIP: 07974  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/970,648  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/378,859  
FILING DATE: 26-JAN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Swode, R Hain  
REGISTRATION NUMBER: 24,864  
REFERENCE/DOCKET NUMBER: 92H8501  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 771 6292  
TELEFAX: (908) 771 6159  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Peptide fragment of human serum albumin  
US-08-970-648-3

Query Match 48.0%; Score 24; DB 3; Length 8;  
Best Local Similarity 80.0%; Pred. No. 3e+05; 0; Indels 0; Gaps 0;  
Matches 4; Conservative 1; Mismatches 0;

QY 4 DENFK 8  
:||||  
Db 4 EENFK 8

RESULT 17  
US-08-952-558-4  
Sequence 4, Application US/08952558  
Patent No. 6638740  
GENERAL INFORMATION:  
APPLICANT: Goodey, Andrew R.  
APPLICANT: Sleep, Darrell  
APPLICANT: Berzenko, Stephen  
APPLICANT: Woodrow, John R.  
APPLICANT: Johnson, Richard A.  
TITLE OF INVENTION: PROCESS OF HIGH PURITY ALBUMIN PRODUCTION  
FILE REFERENCE: CE0111D US  
CURRENT APPLICATION NUMBER: US/08/952,558  
CURRENT FILING DATE: 1999-02-24  
PRIOR APPLICATION NUMBER: PCT/GB96/00449  
PRIOR FILING DATE: 1996-02-29  
PRIOR APPLICATION NUMBER: 378,859

PRIOR FILING DATE: 1995-05-25  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 4  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-08-952-558-4

Query Match 48.0%; Score 24; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DENFK 8  
DB 4 ENFK 8

RESULT 18  
US-08-522-269B-6  
Sequence 6, Application US/08522269B  
Patent No. 5919690

GENERAL INFORMATION:  
APPLICANT: Knapp, Inge Helmer  
APPLICANT: Hjort, Carsten M.  
APPLICANT: Halkier, Torben  
APPLICANT: Kofoed, Lene Venke  
TITLE OF INVENTION: An Alpha-Galactosidase Enzyme  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSER: No. 5919690C No. 5919690disk of No. 5919690th America, Inc.  
STREET: 405 Lexington Avenue, Suite 6400  
CITY: New York  
STATE: New York  
ZIP: 10174-6401  
COUNTRY: U.S.A.

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/522,269B  
FILING DATE: 12-SEP-1995  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Gregg, Valeta A.  
REGISTRATION NUMBER: 37,125  
REFERENCE/DOCKET NUMBER: 3935.204-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212 867 0123  
TELEFAX: 212 867 0298

INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-522-269B-6

Query Match 48.0%; Score 24; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFPD 4  
DB 3 RFPD 6

RESULT 19  
US-09-234-923-6  
Sequence 6, Application US/09294923

Patent No. 6197566  
GENERAL INFORMATION:  
APPLICANT: Knapp, Inge Helmer  
APPLICANT: Hjort, Carsten M.  
APPLICANT: Halkier, Torben  
APPLICANT: Kofoed, Lene Venke  
TITLE OF INVENTION: An Alpha-Galactosidase Enzyme  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSER: No. 6197566C No. 6197566disk of No. 6197566th America, Inc.  
STREET: 405 Lexington Avenue, Suite 6400  
CITY: New York  
STATE: New York  
ZIP: 10174-6401  
COUNTRY: U.S.A.

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/294,923  
FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/522,269  
FILING DATE: 12-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Gregg, Valeta A.  
REGISTRATION NUMBER: 37,125  
REFERENCE/DOCKET NUMBER: 3935.204-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212 867 0123  
TELEFAX: 212 867 0298

INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-294-923-6

Query Match 48.0%; Score 24; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFPD 4  
DB 3 RFPD 6

RESULT 20  
US-08-960-780-59  
Sequence 59, Application US/08960780  
Patent No. 6204435

GENERAL INFORMATION:  
APPLICANT: Feltelson, Jerald S.  
APPLICANT: Schepf, H. Ernest  
APPLICANT: Narva, Kenneth E.  
APPLICANT: Stockhoff, Brian A.  
APPLICANT: Schmitts, James  
APPLICANT: Loewer, David  
APPLICANT: Dullum, Charles Joseph  
APPLICANT: Muller-Cohn, Judy  
TITLE OF INVENTION: No. 6204435e1 Pesticidal Toxins and Nucleotide  
NUMBER OF SEQUENCES: 134  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Saliwanchik, Lloyd & Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville

STATE: FL  
COUNTRY: US  
ZIP: 32606-6669  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/960,780  
FILING DATE: 30-OCT-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/029,848  
FILING DATE: 30-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Saliwanchik, David R.  
REGISTRATION NUMBER: 31,794  
REFERENCE/DOCKET NUMBER: MA-708  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 352-375-8100  
TELEFAX: 352-372-5800  
INFORMATION FOR SEQ ID NO: 59:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-960-780-59

Query Match  
Best Local Similarity 48.0%; Score 24; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDEN 6  
|||  
Db 1 PDEN 4

RESULT 21  
US-09-073-898-59  
Sequence 59, Application US/09073898  
Patent No. 6242669  
GENERAL INFORMATION:  
APPLICANT: Feitelson, Jerald S.  
APPLICANT: Schepf, H. Ernest  
APPLICANT: Narva, Kenneth E.  
APPLICANT: Stochhoff, Brian A.  
APPLICANT: Schmeits, James  
APPLICANT: Loewer, David  
APPLICANT: Dullum, Charles Joseph  
APPLICANT: Muller-cohn, Uduy  
APPLICANT: Stamp, Lisa  
APPLICANT: Morrill, George  
APPLICANT: Finstad-lee, Stacey  
TITLE OF INVENTION: No. 624269e1 Pesticidal Toxins and Nucleotide  
TITLE OF INVENTION: Sequences Which Encode These Toxins  
NUMBER OF SEQUENCES: 144  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: FL  
COUNTRY: US  
ZIP: 32606-6669  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/073,898

FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/029,848  
FILING DATE: 30-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/960,780  
FILING DATE: 30-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Sanders, Jay M.  
REGISTRATION NUMBER: 39,355  
REFERENCE/DOCKET NUMBER: MA-708C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 352-375-8100  
TELEFAX: 352-372-5800  
INFORMATION FOR SEQ ID NO: 59:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-073-898-59

Query Match  
Best Local Similarity 48.0%; Score 24; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDEN 6  
|||  
Db 1 PDEN 4

RESULT 22  
US-09-341-982-21  
Sequence 21, Application US/09341982  
Patent No. 6558671  
GENERAL INFORMATION:  
APPLICANT: SLINGLUFF, Craig L.  
APPLICANT: HUNT, Donald F.  
APPLICANT: ENGELHARD, Victor H.  
APPLICANT: KIRTLSEN, David  
TITLE OF INVENTION: CYSTINE-DEPLETED PEPTIDES RECOGNIZED BY A3-RESTRICTED  
TITLE OF INVENTION: CYTOTOXIC LYMPHOCYTES, AND USES THEREFOR  
FILE REFERENCE: SLINGLUFF-3B  
CURRENT APPLICATION NUMBER: US/09/341,982  
CURRENT FILING DATE: 1999-09-20  
EARLIER APPLICATION NUMBER: PCT/US98/01592  
EARLIER FILING DATE: 1998-01-29  
EARLIER APPLICATION NUMBER: 60/037,781  
EARLIER FILING DATE: 1997-01-31  
NUMBER OF SEQ ID NOS: 104  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 21  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Fragment of  
OTHER INFORMATION: human protein  
US-09-341-982-21

Query Match  
Best Local Similarity 48.0%; Score 24; DB 4; Length 9;  
Best Local Similarity 66.7%; Pred. No. 3e+05;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 DENFTL 9  
|||  
Db 2 DENFTL 7

RESULT 23  
US-09-850-351A-59

Sequence 59, Application US/09850351A  
Patent No. 6656908  
GENERAL INFORMATION:  
APPLICANT: Feltelson, Jerald S.  
Schnepf, H. Ernest  
Narva, Kenneth E.  
Stockhoff, Brian A.  
Schmeits, James  
Loewer, David  
Dullum, Charles Joseph  
Muller-Cohn, Judy  
Stamp, Lisa  
Mortill, George  
TITLE OF INVENTION: Sequences Which Encode These Toxins  
NUMBER OF SEQUENCES: 144  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: FL  
COUNTRY: US  
ZIP: 32606-6669  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/850,351A  
FILING DATE: 07-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/073,898  
FILING DATE: 06-May-1998  
APPLICATION NUMBER: US 08/960,780  
FILING DATE: 30-Oct-1997  
APPLICATION NUMBER: US 60/029,848  
FILING DATE: 30-Oct-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Sanders, Jay M.  
REGISTRATION NUMBER: 39,355  
REFERENCE/DOCKET NUMBER: MA-708CD1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 352-375-8100  
TELEFAX: 352-372-5800  
INFORMATION FOR SEQ ID NO: 59:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 59:  
US-09-850-351A-59  
Query Match 48.0%; Score 24; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDEN 6  
| | | |  
1 PDEN 4  
Db

RESULT 24  
US-09-341-982-36  
Sequence 36, Application US/09341982  
Patent No. 6558671  
GENERAL INFORMATION:  
APPLICANT: SLINGLUFF, Craig L.  
APPLICANT: HUNT, Donald F.  
APPLICANT: ENGELHARD, Victor H.

APPLICANT: KITTLESEN, David  
TITLE OF INVENTION: CYSTEINE-DEPLETED PEPTIDES RECOGNIZED BY A3-RESTRICTED  
FILE REFERENCE: SLINGLUFF-3B  
CURRENT APPLICATION NUMBER: US/09/341,982  
CURRENT FILING DATE: 1999-09-20  
EARLIER APPLICATION NUMBER: PCT/US98/01592  
EARLIER FILING DATE: 1998-01-29  
EARLIER APPLICATION NUMBER: 60/037,781  
EARLIER FILING DATE: 1997-01-31  
NUMBER OF SEQ ID NOS: 104  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 36  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Fragment of  
US-09-341-982-36

Query Match 48.0%; Score 24; DB 4; Length 10;  
Best Local Similarity 66.7%; Pred. No. 1.7e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 DENFTL 9  
| | | |  
3 DENFTL 8  
Db

RESULT 25  
US-09-341-982-58  
Sequence 58, Application US/09341982  
Patent No. 6558671  
GENERAL INFORMATION:  
APPLICANT: SLINGLUFF, Craig L.  
APPLICANT: HUNT, Donald F.  
APPLICANT: ENGELHARD, Victor H.  
APPLICANT: KITTLESEN, David  
TITLE OF INVENTION: CYSTEINE-DEPLETED PEPTIDES RECOGNIZED BY A3-RESTRICTED  
FILE REFERENCE: SLINGLUFF-3B  
CURRENT APPLICATION NUMBER: US/09/341,982  
CURRENT FILING DATE: 1999-09-20  
EARLIER APPLICATION NUMBER: PCT/US98/01592  
EARLIER FILING DATE: 1998-01-29  
EARLIER APPLICATION NUMBER: 60/037,781  
EARLIER FILING DATE: 1997-01-31  
NUMBER OF SEQ ID NOS: 104  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 58  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Fragment of  
US-09-341-982-58

Query Match 48.0%; Score 24; DB 4; Length 11;  
Best Local Similarity 66.7%; Pred. No. 1.9e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 DENFTL 9  
| | | |  
4 DENFTL 9  
Db

RESULT 26  
US-08-934-222-25  
Sequence 25, Application US/08934222  
Patent No. 5928896  
GENERAL INFORMATION:

APPLICANT: EVANS, Herbert J.  
APPLICANT: KINT, R. Manjunatha  
TITLE OF INVENTION: Polypeptides That Include Conformation-  
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction  
TITLE OF INVENTION: Site  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: Suite 500, 3000 K Street NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20007  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,222  
FILING DATE: 19-SEP-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/532,818  
FILING DATE: 03-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/143,364  
FILING DATE: 29-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/051,741  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/DOCKET NUMBER: 040433/0148  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-934-222-25

Query Match 48.0%; Score 24; DB 2; Length 12;  
Best Local Similarity 50.0%; Pred. No. 2.1e+02;  
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PDENFK 8  
Db 5 PDDDFR 10

RESULT 27  
US-08-933-402-25  
Sequence 25, Application US/08933402  
Patent No. 5948887  
GENERAL INFORMATION:  
APPLICANT: EVANS, Herbert J.  
APPLICANT: KINT, R. Manjunatha  
TITLE OF INVENTION: Polypeptides That Include Conformation-  
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction  
TITLE OF INVENTION: Site  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: Suite 500, 3000 K Street NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20007  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/933,402  
FILING DATE: 19-SEP-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/532,818  
FILING DATE: 03-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/143,364  
FILING DATE: 29-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/051,741  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/DOCKET NUMBER: 040433/0148  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-933-402-25

Query Match 48.0%; Score 24; DB 2; Length 12;  
Best Local Similarity 50.0%; Pred. No. 2.1e+02;  
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PDENFK 8  
Db 5 PDDDFR 10

RESULT 28  
US-09-207-621-25  
Sequence 25, Application US/09207621  
Patent No. 5952465  
GENERAL INFORMATION:  
APPLICANT: EVANS, Herbert J.  
APPLICANT: KINT, R. Manjunatha  
TITLE OF INVENTION: Polypeptides That Include Conformation-  
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: Suite 500, 3000 K Street NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20007  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/207,621  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/532,818  
FILING DATE: 03-MAY-1996  
APPLICATION NUMBER: PCT/US94/04294  
FILING DATE: 21-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/143,364  
FILING DATE: 29-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/051,741  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/DOCKET NUMBER: 040433/0148  
INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-09-207-621-25

Query Match 48.0%; Score 24; DB 2; Length 12;  
Best Local Similarity 50.0%; Pred. No. 2.1e+02;  
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDENFK 8  
DB 5 PDDDR 10

RESULT 29  
US-08-532-818-25  
Sequence 25, Application US/08532818

PATENT INFORMATION:  
PATENT NO. 5965698  
APPLICANT: EVANS, Herbert J.  
TITLE OF INVENTION: Polypeptides That Include Conformation-  
CONSTRAINING GROUPS WHICH FLANK A PROTEIN-PROTEIN INTERACTION  
TITLE OF INVENTION: Site  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESS: Foley & Lardner  
STREET: Suite 500, 3000 K Street NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20007

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/532,818  
FILING DATE: 03-MAY-1996  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/04294  
FILING DATE: 21-APR-1994

PRIOR APPLICATION DATA: U.S. 08/143,364  
FILING DATE: 29-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/051,741  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/DOCKET NUMBER: 040433/0148  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-532-818-25

Query Match 48.0%; Score 24; DB 2; Length 12;  
Best Local Similarity 50.0%; Pred. No. 2.1e+02;  
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDENFK 8  
DB 5 PDDDR 10

RESULT 30  
US-08-231-797-25  
Sequence 25, Application US/09231797

PATENT NO. 6084066  
GENERAL INFORMATION:  
APPLICANT: EVANS, Herbert J.  
TITLE OF INVENTION: Polypeptides That Include Conformation-  
CONSTRAINING GROUPS WHICH FLANK A PROTEIN-PROTEIN INTERACTION  
TITLE OF INVENTION: Site  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESS: Foley & Lardner  
STREET: Suite 500, 3000 K Street NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20007

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/231,797  
FILING DATE:  
APPLICATION DATA:  
APPLICATION NUMBER: 08/532,818  
FILING DATE: 03-MAY-1996

APPLICATION NUMBER: PCT/US94/04294  
FILING DATE: 21-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/143,364  
FILING DATE: 29-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/051,741  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/DOCKET NUMBER: 040433/0148  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-09-231-797-25

Query Match 48.0%; Score 24; DB 3; Length 12;  
Best Local Similarity 50.0%; Pred. No. 2.1e+02;  
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDENFK 8  
DB 5 PDDDR 10

RESULT 31  
US-08-934-224-25  
Sequence 25, Application US/08934224

PATENT NO. 6100044  
GENERAL INFORMATION:  
APPLICANT: EVANS, Herbert J.  
TITLE OF INVENTION: Polypeptides That Include Conformation-  
CONSTRAINING GROUPS WHICH FLANK A PROTEIN-PROTEIN INTERACTION  
TITLE OF INVENTION: Site  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESS: Foley & Lardner  
STREET: Suite 500, 3000 K Street NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20007

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,224  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/532,818  
FILING DATE: 03-MAY-1996  
APPLICATION NUMBER: PCT/US94/04294  
FILING DATE: 21-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/143,364  
FILING DATE: 29-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/051,741  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/DOCKET NUMBER: 040433/0148  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-934-224-25

Query Match 48.0%; Score 24; DB 3; Length 12;  
Best Local Similarity 50.0%; Pred. No. 2.1e+02;  
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDENFK 8  
|::|:  
Db 5 PDDDFR 10

RESULT 32

US-08-933-843-25

Sequence 25, Application US/08933843

Patent No. 611069

GENERAL INFORMATION:

APPLICANT: EVANS, Herbert J.

APPLICANT: KINI, R. Manjunatha

TITLE OF INVENTION: Polypeptides That Include Conformation-

TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction

TITLE OF INVENTION: Site

NUMBER OF SEQUENCES: 153

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: Suite 500, 3000 K Street NW

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20007

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/933,843

FILING DATE: 19-SEP-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/532,818

FILING DATE: 03-MAY-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. 08/143,364

FILING DATE: 29-OCT-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. 08/051,741

FILING DATE: 23-APR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/DOCKET NUMBER: 040433/0148  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-933-843-25

Query Match 48.0%; Score 24; DB 3; Length 12;  
Best Local Similarity 50.0%; Pred. No. 2.1e+02;  
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDENFK 8  
|::|:  
Db 5 PDDDFR 10

RESULT 33

US-08-934-223-25

Sequence 25, Application US/08934223

Patent No. 6147189

GENERAL INFORMATION:

APPLICANT: EVANS, Herbert J.

APPLICANT: KINI, R. Manjunatha

TITLE OF INVENTION: Polypeptides That Include Conformation-

TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction

TITLE OF INVENTION: Site

NUMBER OF SEQUENCES: 153

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: Suite 500, 3000 K Street NW

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20007

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/934,223

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/532,818

FILING DATE: 03-MAY-1996

APPLICATION NUMBER: PCT/US94/04294

FILING DATE: 21-APR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. 08/143,364

FILING DATE: 29-OCT-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. 08/051,741

FILING DATE: 23-APR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Isaacson, John P.

REGISTRATION NUMBER: 33,751

REFERENCE/DOCKET NUMBER: 040433/0148

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 12 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-934-223-25

Query Match 48.0%; Score 24; DB 3; Length 12;

Best Local Similarity 50.0%; Pred. No. 2.1e+02;  
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDENFK 8  
|::|:  
Db 5 PDDDFR 10

Db 5 PDDDFR 10

## RESULT 34

US-09-413-492-25  
Sequence 25, Application US/09413492  
Patent No. 6258550

## GENERAL INFORMATION:

APPLICANT: EVANS, Herbert J.

TITLE OF INVENTION: Polypeptides That Include Conformation-

TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction

NUMBER OF SEQUENCES: 153

CORRESPONDENCE ADDRESS:

ADDRESS: Foley &amp; Lardner

STREET: Suite 500, 3000 K Street NW

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20007

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/413,492

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/532,818

FILING DATE: 03-MAY-1996

APPLICATION NUMBER: PCT/US94/04294

FILING DATE: 21-APR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. 08/143,364

FILING DATE: 29-OCT-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. 08/051,741

FILING DATE: 23-APR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Isaacson, John P.

REGISTRATION NUMBER: 33,751

REFERENCE/DOCKET NUMBER: 040433/0148

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 12 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-09-413-492-25

Query Match 48.0%; Score 24; DB 3; Length 12;  
Best Local Similarity 50.0%; Pred. No. 2.1e+02;  
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;QY 3 PDEDFR 8  
Db 5 PDDDFR 10

## RESULT 35

US-08-615-181-91  
Sequence 91, Application US/08615181  
Patent No. 575666

## GENERAL INFORMATION:

APPLICANT: MASAFUMI, TAKIGUCHI

TITLE OF INVENTION: PEPTIDES CAPABLE OF INDUCING IMMUNE

TITLE OF INVENTION: RESPONSE TO HIV AND ANTI-AIDS AGENT FOR PREVENTING AND

NUMBER OF SEQUENCES: 115

CORRESPONDENCE ADDRESS:

ADDRESS: OBLON, SPIVAK, MCCLELLAND, MAIER &amp; NEUSTADT,

ADDRESSEE: P.C.  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

CITY: ARLINGTON

STATE: VA

COUNTRY: USA

ZIP: 22202

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/615,181

FILING DATE: 04-APR-1996

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP94/01756

FILING DATE: 19-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 261302/1993

FILING DATE: 19-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 10-796-0 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-413-3000

TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 91:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

ORIGINAL SOURCE:

ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS

US-08-615-181-91

Query Match 46.0%; Score 23; DB 4; Length 9;  
Best Local Similarity 80.0%; Pred. No. 3e+05;

## RESULT 36

US-09-492-543-73  
Sequence 73, Application US/09492543A  
Patent No. 6316213

## GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of

FILE REFERENCE: D6223CIP-B

CURRENT APPLICATION NUMBER: US/09/492,543A

PRIOR FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: 09/039,211

NUMBER OF SEQ ID NOS: 189

SOFTWARE: WORD 6.0.1 for Macintosh

SEQ ID NO 73

LENGTH: 9

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: Residues 238-246 of the PUMP-1 protein

US-09-492-543-73



Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 ENFKL 9  
:|||||

Db 5 QNFKL 9

RESULT 37

US-09-492-543-101  
; Sequence 101, Application US/09492543A  
; Patent No. 6316213  
; GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of

FILE REFERENCE: D623CIP-B

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: 09/039,211

PRIOR FILING DATE: 03-14-1998

NUMBER OF SEQ ID NOS: 189

SOFTWARE: WORD 6.0.1 for Macintosh

SEQ ID NO 101

LENGTH: 9

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: Residues 238-246 of the PUMP-1 protein

US-09-492-543-101

Query Match

Best Local Similarity 46.0%; Score 23; DB 4; Length 9;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 ENFKL 9  
:|||||

Db 5 QNFKL 9

RESULT 38

US-09-688-188B-113-

; Sequence 113, Application US/09688188B

; Patent No. 6656716

; GENERAL INFORMATION:

APPLICANT: PLOWMAN, GREGORY

APPLICANT: MARTINEZ, RICARDO

APPLICANT: MAYTE, DAVID

TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES

FILE REFERENCE: 038602/0328

CURRENT FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: 09/291,417

PRIOR FILING DATE: 1999-04-14

PRIOR APPLICATION NUMBER: 60/081,784

PRIOR FILING DATE: 1998-04-14

NUMBER OF SEQ ID NOS: 155

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 113

LENGTH: 9

TYPE: PRT

ORGANISM: Homo sapiens

US-09-688-188B-113

Query Match

Best Local Similarity 46.0%; Score 23; DB 4; Length 9;

Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 FPDENFK 8  
|||:::

Db 3 FPKEDYR 9

RESULT 39

US-09-291-417D-113

; Sequence 113, Application US/09291417D

; Patent No. 6660170

; GENERAL INFORMATION:

APPLICANT: PLOWMAN, GREGORY

APPLICANT: MARTINEZ, RICARDO

APPLICANT: MAYTE, DAVID

TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES

FILE REFERENCE: 038602/0328

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: 09/039,211

PRIOR FILING DATE: 03-14-1998

NUMBER OF SEQ ID NOS: 155

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 113

LENGTH: 9

TYPE: PRT

ORGANISM: Homo sapiens

US-09-291-417D-113

Query Match

Best Local Similarity 46.0%; Score 23; DB 4; Length 9;

Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 FPDENFK 8  
|||:::

Db 3 FPKEDYR 9

RESULT 40

US-08-261-206A-10

; Sequence 10, Application US/08261206A

; Patent No. 5574007

; GENERAL INFORMATION:

APPLICANT: Zushi, Mitichitaka

APPLICANT: Gomi, Komakazu

APPLICANT: Yamamoto, Shuji

APPLICANT: Suzuki, Koji

APPLICANT: Matsuda, Akio

TITLE OF INVENTION: A Polypeptide Capable of Interacting

NUMBER OF SEQUENCES: 80

CORRESPONDENCE ADDRESS:

ADDRESSEE: Birch, Stewart, Kolasch & Birch

STREET: 301 N. Washington St.

CITY: Falls Church

STATE: Virginia

COUNTRY: USA

ZIP: 22046-0747

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/261,206A

FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/740,492

FILING DATE: 03-AUG-1991

ATTORNEY/AGENT INFORMATION:

NAME: Svensson, Leonard R.

REGISTRATION NUMBER: 30330

REFERENCE/DOCKET NUMBER: 216-275P

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-241-1300

TELEFAX: 703-241-2848

TELEX: 248345

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-261-206A-10

Query Match 46.0%; Score 23; DB 1; Length 10;  
Best Local Similarity 57.1%; Pred. No. 2.6e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDENFK 8  
DB 4 FPDPCFR 10

RESULT 41  
US-08-261-206A-31  
Sequence 31, Application US/08261206A  
Patent No. 5574007  
GENERAL INFORMATION:  
APPLICANT: Zushi, Mitichitaka  
APPLICANT: Gomi, Komakazu  
APPLICANT: Yamamoto, Shuji  
APPLICANT: Suzuki, Koji  
APPLICANT: Matsuda, Akio  
TITLE OF INVENTION: A Polypeptide Capable of Interacting  
TITLE OF INVENTION: with Thrombin  
NUMBER OF SEQUENCES: 80  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Birch, Stewart, Kolasch & Birch  
STREET: 301 N. Washington St.  
CITY: Falls Church  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22046-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/261,206A  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/740,492  
FILING DATE: 03-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Svenson, Leonard R.  
REGISTRATION NUMBER: 30330  
REFERENCE/DOCKET NUMBER: 216-275P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-241-1300  
TELEFAX: 703-241-2848  
TELEX: 248345  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-261-206A-31

Query Match 46.0%; Score 23; DB 1; Length 10;  
Best Local Similarity 57.1%; Pred. No. 2.6e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDENFK 8  
DB 4 FPDPCFR 10

RESULT 42  
US-08-261-206A-35

Sequence 35, Application US/08261206A  
Patent No. 5574007  
GENERAL INFORMATION:  
APPLICANT: Zushi, Mitichitaka  
APPLICANT: Gomi, Komakazu  
APPLICANT: Yamamoto, Shuji  
APPLICANT: Suzuki, Koji  
APPLICANT: Matsuda, Akio  
TITLE OF INVENTION: A Polypeptide Capable of Interacting  
TITLE OF INVENTION: with Thrombin  
NUMBER OF SEQUENCES: 80  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Birch, Stewart, Kolasch & Birch  
STREET: 301 N. Washington St.  
CITY: Falls Church  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22046-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/261,206A  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/740,492  
FILING DATE: 03-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Svenson, Leonard R.  
REGISTRATION NUMBER: 30330  
REFERENCE/DOCKET NUMBER: 216-275P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-241-1300  
TELEFAX: 703-241-2848  
TELEX: 248345  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-261-206A-35

Query Match 46.0%; Score 23; DB 1; Length 10;  
Best Local Similarity 57.1%; Pred. No. 2.6e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDENFK 8  
DB 4 FPDPCFR 10

RESULT 43  
US-08-261-206A-39  
Sequence 39, Application US/08261206A  
Patent No. 5574007  
GENERAL INFORMATION:  
APPLICANT: Zushi, Mitichitaka  
APPLICANT: Gomi, Komakazu  
APPLICANT: Yamamoto, Shuji  
APPLICANT: Suzuki, Koji  
APPLICANT: Matsuda, Akio  
TITLE OF INVENTION: A Polypeptide Capable of Interacting  
TITLE OF INVENTION: with Thrombin  
NUMBER OF SEQUENCES: 80  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Birch, Stewart, Kolasch & Birch  
STREET: 301 N. Washington St.  
CITY: Falls Church  
STATE: Virginia

Query Match 46.0%; Score 23; DB 1; Length 10;  
Best Local Similarity 57.1%; Pred. No. 2.6e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

COUNTRY: USA  
ZIP: 22046-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/261,206A  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/740,492  
FILING DATE: 03-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Svensson, Leonard R.  
REGISTRATION NUMBER: 30330  
REFERENCE/DOCKET NUMBER: 216-275P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-241-1300  
TELEFAX: 703-241-2848  
TELEX: 248345  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-261-206A-39

Query Match 46.0%; Score 23; DB 1; Length 10;  
Best Local Similarity 57.1%; Pred. No. 2.6e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDENFX 8  
|||  
Db 4 FPDPCFR 10

RESULT 44  
US-08-261-206A-43  
Sequence 43, Application US/08261206A  
Patent No. 5574007  
GENERAL INFORMATION:  
APPLICANT: Zushi, Mitichitaka  
APPLICANT: Gomi, Komakazu  
APPLICANT: Yamamoto, Shuji  
APPLICANT: Suzuki, Koji  
APPLICANT: Matsuda, Akio  
TITLE OF INVENTION: A Polypeptide Capable of Interacting  
TITLE OF INVENTION: with Thrombin  
NUMBER OF SEQUENCES: 80  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Birch, Stewart, Kolasch & Birch  
STREET: 301 N. Washington St.  
CITY: Falls Church  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22046-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/261,206A  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/740,492  
FILING DATE: 03-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Svensson, Leonard R.

REGISTRATION NUMBER: 30330  
REFERENCE/DOCKET NUMBER: 216-275P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-241-1300  
TELEFAX: 703-241-2848  
TELEX: 248345  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-261-206A-43

Query Match 46.0%; Score 23; DB 1; Length 10;  
Best Local Similarity 57.1%; Pred. No. 2.6e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDENFX 8  
|||  
Db 4 FPDPCFR 10

RESULT 45  
US-09-688-188B-79  
Sequence 79, Application US/09688188B  
Patent No. 6656716  
GENERAL INFORMATION:  
APPLICANT: PLOWMAN, GREGORY  
APPLICANT: MARTINEZ, RICARDO  
APPLICANT: WHITE, DAVID  
TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES  
FILE REFERENCES: 038602/0328  
CURRENT APPLICATION NUMBER: US/09/688,188B  
CURRENT FILING DATE: 2000-10-16  
PRIOR APPLICATION NUMBER: 09/291,417  
PRIOR FILING DATE: 1999-04-14  
PRIOR APPLICATION NUMBER: 60/081,784  
PRIOR FILING DATE: 1998-04-14  
NUMBER OF SEQ ID NOS: 155  
SOFTWARE: Patentln Ver. 2.1  
SEQ ID NO 79  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-688-188B-79

Query Match 46.0%; Score 23; DB 4; Length 10;  
Best Local Similarity 42.9%; Pred. No. 2.6e+02;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 FPDENFX 8  
|||  
Db 4 FPDPCFR 10

Search completed: August 30, 2004, 10:57:17  
Job time: 4.55743 secs



GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: August 30, 2004, 10:39:14 ; Search time 13.4088 Seconds  
(without alignments)  
189.646 Million cell updates/sec

Title: US-09-720-469a-7  
Perfect score: 50  
Sequence: 1 RFPDENFKL 9

Scoring table: BLASTSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 309569

Minimum DB seq length: 8  
Maximum DB seq length: 14

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: geneseqp1990s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	100.0	9	3	AAV69927 Human cyc
2	41	82.0	11	3	AAV69926 Human cyc
3	32	64.0	10	7	ADA06843 Solid-phe
4	31	62.0	10	2	AAW44362 Breast ca
5	31	62.0	10	4	AA98714 Human bre
6	30	60.0	9	6	ABR58800 Human bre
7	29	58.0	9	4	AAV68482 Human Bre
8	29	58.0	9	5	ABG67487 Human ADP
9	29	58.0	9	6	ADA23600 Alzheimer
10	29	58.0	9	7	ABR62869 Tumorige
11	29	58.0	9	7	ABR62869 Human 161
12	29	58.0	9	7	ABR62869 Human 161
13	29	58.0	9	7	ABR62869 Human 161
14	29	58.0	10	2	AAV69927 Human cyc
15	29	58.0	10	2	AAV69926 Human cyc
16	29	58.0	10	7	ADA06843 Solid-phe
17	29	58.0	10	2	AAW44362 Breast ca
18	29	58.0	10	4	AA98714 Human bre
19	29	58.0	10	4	AA98714 Human bre
20	29	58.0	13	5	ABP46673 Human Bly
21	29	58.0	14	5	ABP46673 Human Bly
22	29	58.0	14	5	ABP46673 Human Bly
23	28	56.0	9	6	ABJ42183 151P3D4 C
24	28	56.0	9	6	ABJ42183 151P3D4 C
25	28	56.0	9	6	ABJ42183 151P3D4 C

26	28	56.0	9	6	ABJ45672 151P3D4 C
27	28	56.0	9	6	ABJ47747 151P3D4 C
28	28	56.0	9	6	ABJ49116 151P3D4 C
29	28	56.0	9	6	ABJ41779 151P3D4 C
30	28	56.0	9	6	ABJ41872 151P3D4 C
31	28	56.0	9	6	ABJ47004 151P3D4 C
32	28	56.0	9	6	ABJ39404 151P3D4 C
33	28	56.0	9	6	ABJ44281 151P3D4 C
34	28	56.0	9	6	ABJ45005 151P3D4 C
35	28	56.0	9	6	ABJ45032 151P3D4 C
36	28	56.0	9	6	ABJ48393 151P3D4 C
37	28	56.0	9	6	ABJ43122 151P3D4 C
38	28	56.0	9	6	ABJ46322 151P3D4 C
39	28	56.0	9	6	ABJ47111 151P3D4 C
40	28	56.0	9	6	ABJ48392 151P3D4 C
41	28	56.0	9	6	ABJ39852 151P3D4 C
42	28	56.0	9	6	ABJ41450 151P3D4 C
43	28	56.0	9	6	ABJ46607 151P3D4 C
44	28	56.0	9	6	ABJ40977 151P3D4 C
45	28	56.0	9	6	ABJ49160 151P3D4 C

## ALIGNMENTS

RESULT 1  
AAV69927  
ID AAV69927 standard; peptide, 9 AA.

AC AAV69927;  
DT 11-APR-2000 (first entry)

DE Human cyclophilin B peptide fragment #7.

KM Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;  
HLA antigen; diagnosis; tumour; therapy.

OS Homo sapiens.

PN WO967288-A1.

PD 29-DEC-1999.

PF 24-JUN-1999; 99WO-JP003360.

PR 25-JUN-1998; 98JP-00178449.

PA (SUMU) SUMITOMO PHARM CO LTD.

PI (ITOH) ITOH K.

PT Itoh K, Gomi S,

DR WPI, 2000-116932/10.

PT Tumor antigen peptides derived from cyclophilin B for treatment and  
diagnosis of tumors.

PS Claim 4; Page 51; 64pp; Japanese.

CC This sequence represents a cyclophilin B peptide of the invention. The  
peptides are tumour antigen peptides derived from cyclophilin B, that  
recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The  
peptides are used for the treatment and diagnosis of tumours

SO Sequence 9 AA:

Query Match 100.0%; Score 50; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 RFPDENFKL 9  
|||||||

Db 1 RPPDENFXL 9

# RESULT 2

AAV69926  
ID AAV69926 standard; peptide; 11 AA.

AC AAV69926;

DT 11-APR-2000 (first entry)

DE Human cyclophilin B peptide fragment #6.

KM Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;  
KW HLA antigen; diagnosis; tumour; therapy.

OS Homo sapiens.

XX WO9967288-A1.

PD 29-DEC-1999.

PF 24-JUN-1999; 99WO-JP003360.

PR 25-JUN-1998; 98JP-00178449.

PA (SUMU) SUMITOMO PHARM CO LTD.  
(ITOH) ITOH K.

PI Itoh K, Gomi S;

DR WPI; 2000-116932/10.

PT Tumour antigen peptides derived from cyclophilin B for treatment and  
diagnosis of tumours.

PS Claim 4; Page 50; 64pp; Japanese.

CC This sequence represents a cyclophilin B peptide of the invention. The  
CC peptides are tumour antigen peptides derived from cyclophilin B, that  
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The  
CC peptides are used for the treatment and diagnosis of tumours

XX Sequence 11 AA;

Query Match 82.0%; Score 41; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.42;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPPDENF 7  
Db 5 RPPDENF 11

# RESULT 3

ADA06843  
ID ADA06843 standard; peptide; 10 AA.

AC ADA06843;

DT 06-NOV-2003 (first entry)

DE Solid-phase synthesis produced organic peptide #5.

KM Aldehyde functionalised support material; solid-phase synthesis;  
KW organic compound; acid; thioacid; thioester; alcohol;  
XX disubstituted amide; aldehyde.

OS Synthetic.

XX Key location/Qualifiers  
FT Modified-site 1  
FT /label= OTHER

FT /note= "OTHER= "Fmoc-Arg"  
FT Misc-difference 2  
FT /note= "D-form residue"  
FT Modified-site 10  
FT /label= OTHER  
FT /note= "OTHER= "Ala-OAl"  
XX

PN US6566494-B1.

PD 20-MAY-2003.

PF 11-MAY-1999; 99US-00309828.

PR 18-JUN-1996; 96US-00655509.

XX (MIND) UNIV MINNESOTA.

XX Jensen KJ, Barany G, Songster MF, Albericio F, Alsina J;  
PI Vagner J;

DR WPI; 2003-596202/56.

PT New aldehyde functionalized support material used for solid phase organic  
synthesis.

PS Example 14; Col 18; 18pp; English.

CC The invention is related to an aldehyde functionalised support material.  
CC The aldehyde functionalised support material is used for solid-phase  
CC synthesis of organic compounds, particularly peptides. The organic  
CC compounds can have a variety of C-terminal functionalities e.g. acids,  
CC thioacids, thioesters, alcohols, disubstituted amides and aldehydes can  
CC be produced. This sequence represents an organic peptide prepared by  
CC solid-phase synthesis, using the support material of the invention.

XX Sequence 10 AA;

Query Match 64.0%; Score 32; DB 7; Length 10;  
Best Local Similarity 50.0%; Pred. No. 20;  
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPPDENFX 8  
Db 1 RPPDENFX 8

# RESULT 4

AAW44362  
ID AAW44362 standard; peptide; 10 AA.

AC AAW44362;

DT 28-MAY-1998 (first entry)

DE Breast cancer-associated protein fragment BC-8 SEQ ID NO:8.

KM Human; breast cancer-associated protein; nuclear matrix protein;  
KW detection; diagnosis; antibody.

OS Homo sapiens.

PN WO9746884-A1.

PD 11-DEC-1997.

PF 03-JUN-1997; 97WO-US009529.

PR 05-JUN-1996; 96US-00658639.

XX (MATR-) MATRITECH INC.

XX Keesee SK, Obar R, Wu Y;

DR WPI; 1998-042336/04.  
XX Diagnosing breast cancer by detecting a breast cancer-associated protein  
PT - allows early and reliable diagnosis and treatment monitoring, and  
PT antibody or inhibitory compounds useful for treating breast cancer.  
XX  
PS Claim 10; Page 30; 47pp; English.  
XX  
The present sequence represents a breast cancer-associated protein  
CC fragment for use in a method for diagnosing breast cancer in tissue or  
CC body fluid by detecting one or more breast cancer-associated protein(s).  
CC Alternatively a nucleic acid encoding a breast cancer-associated protein  
CC is detected in the sample by the use of a nucleic acid probe. The breast  
CC cancer-associated proteins, encoding nucleic acids and antibodies are  
CC useful in diagnostic assays and kits for breast cancer detection. The  
CC proteins are also useful in screening for inhibitory compounds and  
CC monitoring effectiveness of treatments. The antibody, or pharmaceutical  
CC compositions containing the antibody or the inhibitory compound, can be  
CC administered to patients to treat breast cancer. The methods allow  
CC reliable and early diagnosis of breast cancer, or prediction of its  
CC onset, by detection of specific markers expressed in breast tumour cells  
CC but not in non-cancerous breast cells  
XX  
SQ Sequence 10 AA;  
Query Match 62.0%; Score 31; DB 2; Length 10;  
Best Local Similarity 66.7%; Pred. No. 30;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 RFPDENFKL 9  
:| |||||  
Db 1 KFDDENFIL 9  
RESULT 5  
AAB98714  
ID AAB98714 standard; peptide; 10 AA.  
XX  
AC AAB98714;  
XX  
XX 29-AUG-2001 (first entry)  
XX  
DE Human breast cancer-associated protein BC-8 peptide, SEQ ID NO:8.  
XX  
KM Human breast cancer-associated protein; BC-8; marker protein;  
XX nuclear matrix protein; diagnosis; detection; tumour.  
XX  
OS Homo sapiens.  
XX  
PN US6218131-B1.  
XX  
PD 17-APR-2001.  
XX  
PF 06-OCT-1997; 97US-00944604.  
XX  
PR 05-JUN-1996; 96US-00658639.  
XX  
PA (MATR-) MATRITECH INC.  
XX  
PI Keesee SK, Obar R, Wu Y;  
XX  
XX WPI; 2001-396355/42.  
XX  
PT Diagnosing or detecting breast cancer in an individual comprises  
PT detecting the presence of breast cancer-associated proteins in a  
PT biological sample.  
XX  
PS Claim 9; Col 8; 30pp; English.  
XX  
XX The invention relates to novel human breast cancer-associated proteins,  
CC and their use in diagnosing and detecting breast cancer. The breast  
CC cancer-associated proteins of the invention are nuclear matrix proteins  
CC designated BC-2 (AAB98720), BC-8 isoform A (BC-8A, AAB98721) and CC BC-8

CC isoform B (BC-8B, AAB98722), although 6 other breast cancer-associated  
CC nuclear matrix proteins (BC-1, BC-3, BC-4, BC-5, BC-6, and BC-7) were  
CC also isolated (sequences not given in the specification). The novel  
CC breast cancer-associated proteins are present in the nuclear matrix of  
CC breast cancer cells, but are not present in the nuclear matrix of cells  
CC from normal breast tissue. The invention also encompasses fragments of  
CC the breast cancer-associated proteins (AAB98709-AAB98716), and methods  
CC for their use in breast cancer diagnosis. The breast cancer marker  
CC proteins of the invention or fragments thereof may be detected in a  
CC sample of breast tissue or blood from an individual. Isolated breast  
CC cancer-associated proteins may also be used to prepare antibodies,  
CC particularly monoclonal antibodies, which may be used to detect or  
CC diagnose breast cancer. Nucleic acids encoding the breast cancer-  
CC associated proteins may also be used in the diagnosis and detection of  
CC breast cancer, and in the isolation of DNA or protein sequences which may  
CC interact with breast cancer-associated nuclear matrix proteins. Sequences  
CC AAB98712-AAB98716 represent specifically claimed fragments of breast  
CC cancer-associated protein BC-8  
XX  
SQ Sequence 10 AA;  
Query Match 62.0%; Score 31; DB 4; Length 10;  
Best Local Similarity 66.7%; Pred. No. 30;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 RFPDENFKL 9  
:| |||||  
Db 1 KFDDENFIL 9  
RESULT 6  
AAB98800  
ID AAB98800 standard; peptide; 9 AA.  
XX  
AC AAB98800;  
XX  
XX 11-JUL-2003 (first entry)  
XX  
DE Alzheimer's Disease-associated protein isoform, AAI-333, SEQ ID 118.  
XX  
XX  
KM Nootropic; Neuroprotective; Alzheimer's disease; API; human;  
XX Alzheimer's Disease-associated protein isoform.  
XX  
OS Homo sapiens.  
XX  
PN WO2003028543-A2.  
XX  
PD 10-APR-2003.  
XX  
PF 03-OCT-2002; 2002WO-US031642.  
XX  
PR 03-OCT-2001; 2001US-0326708P.  
XX  
PA (PFIZ ) PFIZER PROD INC.  
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
XX  
PI Durham LK, Friedman DL, Herath HVA, Kimmel LH, Parekh RB;  
PI Potter DM, Rohlf C, Silber BM, Snyder PJ, Soares HD, Stiger TR,  
PI Sunderland PT, Townsend RR, White WF, Williams SA;  
XX  
XX WPI; 2003-371957/35.  
XX  
XX Screening or diagnosing of Alzheimer's disease (AD) determine the stage  
PT or severity of AD in a subject, comprises analyzing a test sample of body  
PT fluid from the subject by 2-dimensional electrophoresis.  
XX  
PS Claim 2; Page 34; 179pp; English.  
XX  
XX The present invention relates to methods for screening or diagnosing  
CC Alzheimer's disease (AD) to determine the stage or severity of AD in a  
CC subject, to identify subject at risk of developing AD, or to monitor the  
CC effect of therapy administered. The methods comprise analysing a test  
CC sample of body fluid by 2-dimensional electrophoresis to generate a 2-

CC dimensional array of AD-associated features (AFs). The method  
CC alternatively comprises quantitatively detecting in a sample of body  
CC fluid from the subject, one or more AD-associated protein isoforms (APIs;  
CC ABR58710-ABR59164)  
XX  
SQ Sequence 9 AA;

Query Match 60.0%; Score 30; DB 6; Length 9;  
Best Local Similarity 75.0%; Pred. No. 1.4e+06;  
Matches 6; Conservative. 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 FPDENPXL 9  
DB 1 FEDENPFL 8

RESULT 7  
ID AAV68482 standard; peptide: 9 AA.  
XX  
AC AAV68482;  
XX  
DT 16-JAN-2002 (first entry)  
XX  
DE Human Breast cancer-associated protein isoform, BPI-270 peptide #2.  
XX  
KW Human; Breast cancer-associated protein isoform; breast cancer;  
KW Immunogen; cytosolic; BPI; tryptic digest peptide.  
XX  
OS Homo sapiens.  
XX  
PN MO200171357-A2.  
XX  
PD 27-SEP-2001.  
XX  
PF 20-MAR-2001; 2001WO-GB001219.  
XX  
PR 20-MAR-2000; 2000GB-00006695.  
XX  
PR 24-MAR-2000; 2000GB-00007265.  
XX  
FA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
XX  
PI Herath HMAc, O'hare MJ, Parekh RB, Waterfield MD;  
XX  
DR WPI; 2001-611532/70.  
XX

PT Identifying proteins for clinical screening, diagnosis and prognosis of  
PT breast cancer, comprises detecting Breast Cancer-Associated Protein  
PT Isoforms (BPIs) using two-dimensional electrophoresis.  
XX  
PS Claim 9; Page 53; 197pp; English.

XX The invention relates to diagnosing, determining the stage or severity,  
CC or identifying the risk of a subject developing cancer (especially breast  
CC cancer), or monitoring the effect of therapy on a subject with cancer,  
CC comprising analysing a test sample using two-dimensional electrophoresis  
CC and detecting Breast Cancer-Associated Protein Isoforms (BPIs). The  
CC methods disclosed are used for the diagnosis and prognosis of breast  
CC cancer, for determining the severity of breast cancer, and for  
CC identifying a subject at risk of developing breast cancer, and for  
CC against the binding domain of a BPI, the binding domain of a BPI, a  
CC nucleic acid encoding a BPI, or a nucleic acid that inhibits the function  
CC of a BPI can be incorporated into a pharmaceutical composition for  
CC treating or preventing breast cancer. The method use sensitive and  
CC specific biomarkers provide early diagnosis of breast cancer, and the  
CC compositions are more potent, specific, and has a more rapid effect with  
CC fewer side effects than other prior art methods. The present sequence is  
CC a tryptic digest peptide from a BPI of the invention  
XX  
SQ Sequence 9 AA;

Query Match 58.0%; Score 29; DB 4; Length 9;

Best Local Similarity 75.0%; Pred. No. 1.4e+06;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 FPDENPXL 9  
DB 1 FEDENPFL 8

RESULT 8  
ID ABG67487 standard; peptide: 9 AA.  
XX  
AC ABG67487;  
XX  
DT 07-OCT-2002 (first entry)  
XX  
DE Human ADPI tryptic digest peptide #196.  
XX  
KW Human; Alzheimer's disease; AD; brain tissue; ADPI; ADPI;  
KW Alzheimer's disease-associated feature; neuroprotective;  
KW Alzheimer's disease-associated protein isoform; neurotropic;  
KW ADPI tryptic digest peptide.  
XX  
OS Homo sapiens.  
XX  
PN MO200246767-A2.  
XX  
PD 13-JUN-2002.  
XX  
PF 29-NOV-2001; 2001WO-GB005289.  
XX  
PR 08-DEC-2000; 2000US-0254431P.  
XX  
FA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
XX  
PI Herath HMAc, Parekh RB, Rohlf C;  
XX  
DR WPI; 2002-508575/54.  
XX

PT Screening, diagnosis or prognosis of Alzheimer's disease in subject,  
PT comprises detecting Alzheimer disease-associated features or Alzheimer  
PT disease-associated protein isoforms in brain tissue from the subject.  
XX  
PS Claim 7; Page 72; 427pp; English.

XX The present invention relates to methods and compositions for the  
CC screening, diagnosis or prognosis of Alzheimer's disease (AD) in a  
CC subject. The method comprises analysing a sample of brain tissue from a  
CC subject by 2D electrophoresis to generate a 2D array of Alzheimer's  
CC disease-associated features (ADFs), whose relative abundance correlates  
CC with the presence, absence, stage or severity of AD and comparing the  
CC abundance of each feature with the abundance of that chosen feature in  
CC brain tissue from persons free from AD. The invention also describes in  
CC Alzheimer's disease-associated protein isoforms (ADPIs) detectable in  
CC brain tissue. The methods and compositions of the invention are useful  
CC for the screening, diagnosis or prognosis of AD in a subject, for  
CC determining the stage or severity of AD in a subject, for identifying a  
CC subject at risk of developing AD, or for monitoring the effect of therapy  
CC administered to a subject having AD. Antibodies capable of binding to  
CC ADPIs are useful for treating or preventing AD, and for determining the  
CC efficacy of a given treatment regime. An agent that modulates the  
CC activity of ADPI is useful in the manufacture of a medicament for the  
CC treatment or prevention of AD in a subject. ABG67292-ABG68038 represent  
CC human ADPI tryptic digest peptides  
XX  
SQ Sequence 9 AA;

Query Match 58.0%; Score 29; DB 5; Length 9;  
Best Local Similarity 75.0%; Pred. No. 1.4e+06;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 FPDENPXL 9  
DB 1 FEDENPFL 8



Db 1 FEDENFTL 8

RESULT 9  
ADA23600  
ADA23600 standard; peptide; 9 AA.

XX  
AC ADA23600;  
XX  
XX 20-NOV-2003 (first entry)  
XX  
DE Alzheimer's disease-associated protein isoform tryptic peptide #209.  
XX human; Alzheimer's disease; vascular dementia; Lewy body dementia;  
XX schizophrenia; Parkinson's disease; multiple sclerosis; depression;  
XX Alzheimer's disease-associated protein isoform; ADPI.  
XX  
OS Homo sapiens.  
XX  
XX US2003064411-A1.  
XX  
XX 03-APR-2003.  
XX  
XX 10-DEC-2001; 2001US-00014340.  
XX  
XX 08-DEC-2000; 2000US-0254431P.  
XX  
XX (HERA/) HERATH H M A C.  
XX (PARE/) PAREKH R B.  
XX (ROHL/) ROHLFF C.  
XX  
XX Herath HMC, Parekh RB, Rohlf C;  
XX WPI; 2003-540784/51.  
XX  
XX Screening, diagnosis or prognosis of Alzheimer's disease in subject,  
XX PT involves analyzing test sample of brain tissue from subject, and  
XX PT comparing feature in test sample with that of person(s) free from  
XX Alzheimer's disease.  
XX  
XX Disclosure; SEQ ID NO 209; 115pp; English.  
XX  
XX The invention relates to a method of screening or diagnosing Alzheimer's  
XX disease in a subject. The method is useful for screening, diagnosis or  
XX prognosis of Alzheimer's disease in a subject for determining the stage  
XX of severity of Alzheimer's disease in a subject, for identifying a  
XX subject at risk of developing Alzheimer's disease, or for monitoring the  
XX effect of therapy administered to a subject having Alzheimer's disease.  
XX The method is also useful in treating vascular dementia, Lewy body  
XX dementia, schizophrenia, Parkinson's disease, multiple sclerosis or  
XX depression. The inventive method identifies sensitive and specific  
XX biomarkers for the diagnosis of Alzheimer's disease in living subjects.  
XX It provides therapeutic agents for Alzheimer's disease that works  
XX quickly, potentially, specifically with fewer side effects. The present  
XX sequence represents the amino acid sequence of a Alzheimer's disease-  
XX associated protein isoform tryptic peptide.  
XX  
XX Sequence 9 AA;  
XX  
XX Query Match 58.0%; Score 29; DB 6; Length 9;  
XX Best Local Similarity 75.0%; Pred. No. 1.4e+06;  
XX Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX  
XX 04-DEC-2003 (first entry)  
XX  
XX Tumorigenesis, metastasis-associated T cell cyclophilin peptide.  
XX  
XX  
XX Cyclophilin; peptidyl-prolyl cis-trans isomerase; enzyme; tumorigenesis;  
XX metastasis; cancer; diagnosis; human.  
XX  
XX Homo sapiens.  
XX  
XX WO2003060522-A1.  
XX  
XX 24-JUL-2003.  
XX  
XX 28-DEC-2002; 2002WO-KR002469.  
XX  
XX 29-DEC-2001; 2001KR-00088090.  
XX  
XX (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.  
XX  
XX Ko JH, Hwang SY, Sohn H, Oh S, Lee JH, Lee SC, Yoo J, Lee D;  
XX WPI; 2003-646050/61.  
XX  
XX  
XX diagnosing cancers by measuring the changes of N-linked sugar chains of  
XX PT proteins related to tumorigenesis and metastasis, including cancers of  
XX PT the large intestine, stomach, lung, liver, uterus, breast and pancreas.  
XX  
XX Example 3; Page 42; 49pp; English.  
XX  
XX The present sequence is a peptide fragment of T cell cyclophilin  
XX (peptidyl-prolyl cis-trans isomerase). Changes in glycosylation of this  
XX protein are associated with metastasis and tumorigenesis. The protein  
XX has 3 preserved N-linked sugar chain sites. A method for diagnosing  
XX cancer involves measuring changes of sugar chains of proteins related to  
XX tumorigenesis and metastasis. The changes are especially changes of sugar  
XX chain branches of N-linked beta-1,6-N-acetylglucosamine. The protein is  
XX prostate-derived factor, peptidyl-prolyl cis-trans isomerase, galectin  
XX binding protein, L3 antigen, Mac-2-binding protein, serum protein 90K,  
XX tumour associated antigen 90K, TIMP-1 and a novel, unidentified protein.  
XX The cancer is large intestine cancer, stomach cancer, lung cancer, liver  
XX cancer, uterine cancer, breast cancer and pancreas cancer  
XX  
XX Sequence 9 AA;  
XX  
XX Query Match 58.0%; Score 29; DB 7; Length 9;  
XX Best Local Similarity 75.0%; Pred. No. 1.4e+06;  
XX Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX  
XX 2 FEDENFTL 9  
XX 1 FEDENFTL 8

Db

RESULT 11  
ADE66799  
ADE66799 standard; peptide; 9 AA.

XX  
XX ADE66799;  
XX  
XX 29-JAN-2004 (first entry)  
XX  
XX Human 161P2P10B protein-related peptide 806.  
XX  
XX 161P2P10B; cancer; cyrostatic; gene therapy; vaccine; human.  
XX  
XX Homo sapiens.  
XX  
XX WO2003040340-A2.  
XX  
XX 15-MAY-2003.  
XX  
XX 07-NOV-2002; 2002WO-US036002.

XX 07-NOV-2001; 2001US-00005480.  
 PR 31-JAN-2002; 2002US-00062109.  
 XX  
 XX (AGEN-) AGENSYS INC.  
 XX  
 XX Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM,  
 PI Morrison RK, Chailita-Eld PM;  
 XX WPI; 2003-441560/41.  
 DR  
 XX  
 XX A composition for diagnosing, preventing and treating cancer (e.g.  
 PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides  
 PT and polypeptides.  
 XX  
 XX Claim 13; Page 151; 135pp; English.  
 XX  
 XX This invention relates to a novel composition which comprises a substance  
 CC that modulates the status of a novel human protein (161P2F10B) and its  
 CC variants having a sequence of 875 amino acids provided in the  
 CC specification. The protein of the invention is over-expressed in certain  
 CC cancers. The compounds of the invention may have cytostatic activity and  
 CC the sequence of the 161P2F10B protein, and the gene which encodes it, may  
 CC be useful for gene therapy or the development of a vaccine. The  
 CC composition and methods of the invention are useful in diagnosing,  
 CC preventing and treating cancer. The present sequence is the amino acid  
 CC sequence of a peptide which is derived from the sequence of the human  
 CC 161P2F10B protein and which may be used in the development of the  
 CC compounds of the invention.  
 CC  
 XX Sequence 9 AA;  
 SQ  
 Query Match 58.0%; Score 29; DB 7; Length 9;  
 Best Local Similarity 62.5%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 RFPDENFK 8  
 | | | | |  
 2 RKPDQHF 9  
 DB  
 RESULT 12  
 ADE68459  
 ID ADE68459 standard; peptide; 9 AA.  
 XX  
 XX ADE68459;  
 AC  
 XX 29-JAN-2004 (first entry)  
 DT  
 XX Human 161P2F10B protein-related peptide 2464.  
 DE  
 XX 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.  
 KM  
 XX Homo sapiens.  
 OS  
 XX WO2003040340-A2.  
 PN  
 XX 15-MAY-2003.  
 PD  
 XX 07-NOV-2002; 2002WO-US036002.  
 PF  
 XX 07-NOV-2001; 2001US-00005480.  
 PR  
 XX 31-JAN-2002; 2002US-00062109.  
 PA  
 XX (AGEN-) AGENSYS INC.  
 XX  
 XX Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM,  
 PI Morrison RK, Chailita-Eld PM;  
 XX WPI; 2003-441560/41.  
 DR  
 XX A composition for diagnosing, preventing and treating cancer (e.g.  
 PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides

PT and polypeptides.  
 XX  
 XX Claim 13; Page 164; 135pp; English.  
 XX  
 XX This invention relates to a novel composition which comprises a substance  
 CC that modulates the status of a novel human protein (161P2F10B) and its  
 CC variants having a sequence of 875 amino acids provided in the  
 CC specification. The protein of the invention is over-expressed in certain  
 CC cancers. The compounds of the invention may have cytostatic activity and  
 CC the sequence of the 161P2F10B protein, and the gene which encodes it, may  
 CC be useful for gene therapy or the development of a vaccine. The  
 CC composition and methods of the invention are useful in diagnosing,  
 CC preventing and treating cancer. The present sequence is the amino acid  
 CC sequence of a peptide which is derived from the sequence of the human  
 CC 161P2F10B protein and which may be used in the development of the  
 CC compounds of the invention.  
 CC  
 XX Sequence 9 AA;  
 SQ  
 Query Match 58.0%; Score 29; DB 7; Length 9;  
 Best Local Similarity 62.5%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 RFPDENFK 8  
 | | | | |  
 2 RKPDQHF 9  
 DB  
 RESULT 13  
 ADE68822  
 ID ADE68822 standard; peptide; 9 AA.  
 XX  
 XX ADE68822;  
 AC  
 XX 29-JAN-2004 (first entry)  
 DT  
 XX Human 161P2F10B protein-related peptide 2827.  
 DE  
 XX 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.  
 KM  
 XX Homo sapiens.  
 OS  
 XX WO2003040340-A2.  
 PN  
 XX 15-MAY-2003.  
 PD  
 XX 07-NOV-2002; 2002WO-US036002.  
 PF  
 XX 07-NOV-2001; 2001US-00005480.  
 PR  
 XX 31-JAN-2002; 2002US-00062109.  
 PA  
 XX (AGEN-) AGENSYS INC.  
 XX  
 XX Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM,  
 PI Morrison RK, Chailita-Eld PM;  
 XX WPI; 2003-441560/41.  
 DR  
 XX A composition for diagnosing, preventing and treating cancer (e.g.  
 PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides  
 PT and polypeptides.  
 XX  
 XX Claim 13; Page 166; 135pp; English.  
 XX  
 XX This invention relates to a novel composition which comprises a substance  
 CC that modulates the status of a novel human protein (161P2F10B) and its  
 CC variants having a sequence of 875 amino acids provided in the  
 CC specification. The protein of the invention is over-expressed in certain  
 CC cancers. The compounds of the invention may have cytostatic activity and  
 CC the sequence of the 161P2F10B protein, and the gene which encodes it, may  
 CC be useful for gene therapy or the development of a vaccine. The  
 CC composition and methods of the invention are useful in diagnosing,  
 CC preventing and treating cancer. The present sequence is the amino acid

CC sequence of a peptide which is derived from the sequence of the human  
 CC 161P2F10B protein and which may be used in the development of the  
 CC compounds of the invention.

XX  
 SQ Sequence 9 AA;

Query Match 58.0%; Score 29; DB 7; Length 9;  
 Best Local Similarity 62.5%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 RFPDENFK 8  
 Db 2 RKPDQHF 9

RESULT 14

AA49843  
 ID AA49843 standard; protein; 10 AA.

AC AA49843;

XX 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 18-OCT-1994 (first entry)

XX GB fragment corresp. to EcoRV site area.

XX Type A; type B; portable intron; Marek's disease virus; MDV; B antigen;

XX A antigen; pin(E/K); pin(F/P); exon.

XX Marek disease virus type 1.

XX WO9405784-A1.

XX 17-MAR-1994.

XX 27-AUG-1993; 93WO-US008067.

XX 27-AUG-1992; 92US-00936423.

XX (USDA) US SEC OF AGRIC.

XX Relilly JD, Silva RF;

XX WPI: 1994-101189/12.

XX N-PSDB; AAQ44505.

XX Portable intron for use as a vector for gene insertion - can be used to

XX express foreign genes in a host or correct defects in the host's

XX expression of a gene.

XX Example 5; Fig 12A; 89p; English.

XX Example 5 describes the insertion of type A portable intron into B

XX antigen gene. AAQ44505 comprises the coding sequence surrounding the

XX EcoRV site in GB. AAQ44506 comprises the coding sequence after the

XX inserted type A portable intron is spliced out of GB. The amino acids

XX contributed by the type A portable intron exon sequences remain in GB

XX after RNA splicing. The translational reading frame is not disrupted.

XX (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-AUG-2003 to

XX correct OS field.)

XX Sequence 10 AA;

Query Match 58.0%; Score 29; DB 2; Length 10;

Best Local Similarity 57.1%; Pred. No. 73;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RFPDENFK 8

Db 4 YPCDNFK 10

RESULT 15

ADE69600  
 ID ADE69600 standard; peptide; 10 AA.

XX ADE69600;

XX 29-JAN-2004 (first entry)

XX Human 161P2F10B protein-related peptide 3605.

XX 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.

XX Homo sapiens.

XX WO2003040340-A2.

XX 15-MAY-2003.

XX 07-NOV-2002; 2002WO-US036002.

XX 07-NOV-2001; 2001US-00005480.

XX 31-JAN-2002; 2002US-00062109.

XX (AGEN-) AGENSYS INC.

XX Jakobovits A, Raitano AB, Paris M, Hubert RS, Ge W, Morrison KM;

XX Morrison RK, Challita-Eld PM;

XX WPI: 2003-441560/41.

XX A composition for diagnosing, preventing and treating cancer (e.g.

XX prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides

XX and polypeptides.

XX Claim 13; Page 171; 135p; English.

XX This invention relates to a novel composition which comprises a substance

XX that modulates the status of a novel human protein (161P2F10B) and its

XX variants having a sequence of 875 amino acids provided in the

XX specification. The protein of the invention is over-expressed in certain

XX cancers. The compounds of the invention may have cytostatic activity and

XX the sequence of the 161P2F10B protein, and the gene which encodes it, may

XX be useful for gene therapy or the development of a vaccine. The

XX composition and methods of the invention are useful in diagnosing,

XX preventing and treating cancer. The present sequence is the amino acid

XX sequence of a peptide which is derived from the sequence of the human

XX 161P2F10B protein and which may be used in the development of the

XX compounds of the invention.

XX Sequence 10 AA;

Query Match 58.0%; Score 29; DB 7; Length 10;

Best Local Similarity 62.5%; Pred. No. 73;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RFPDENFK 8

Db 3 RKPDQHF 10

RESULT 16

ADE66863  
 ID ADE66863 standard; peptide; 10 AA.

XX ADE66863;

XX 29-JAN-2004 (first entry)

XX Human 161P2F10B protein-related peptide 870.

XX 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.

XX Homo sapiens.

XX W02003040340-A2.  
XX 15-MAY-2003.  
XX 07-NOV-2002; 2002WO-US036002.  
XX 07-NOV-2001; 2001US-00005480.  
XX 31-JAN-2002; 2002US-00062109.  
XX (AGEN-) AGENSYS INC.  
XX Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;  
XX Morrison RK, Challita-Eid PM;  
XX WPI; 2003-441560/41.  
XX A composition for diagnosing, preventing and treating cancer (e.g.  
XX prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides  
XX and polypeptides.  
XX Claim 13; Page 152; 135pp; English.  
XX This invention relates to a novel composition which comprises a substance  
XX that modulates the status of a novel human protein (161P2F10B) and its  
XX variants having a sequence of 875 amino acids provided in the  
XX specification. The protein of the invention is over-expressed in certain  
XX cancers. The compounds of the invention may have cytostatic activity and  
XX the sequence of the 161P2F10B protein, and the gene which encodes it, may  
XX be useful for gene therapy or the development of a vaccine. The  
XX composition and methods of the invention are useful in diagnosing,  
XX preventing and treating cancer. The present sequence is the amino acid  
XX sequence of a peptide which is derived from the sequence of the human  
XX 161P2F10B protein and which may be used in the development of the  
XX compounds of the invention.  
XX Sequence 10 AA;  
XX  
XX Query Match 58.0%; Score 29; DB 7; Length 10;  
XX Best Local Similarity 62.5%; Pred. No. 73;  
XX Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
XX  
XX 1 RFPDENFK 8  
XX |||:|  
XX 3 RKPQDHFK 10  
XX  
XX RESULT 17  
XX ADE69184  
XX ID ADE69184 standard; peptide; 10 AA.  
XX ADE69184;  
XX 29-JAN-2004 (first entry)  
XX Human 161P2F10B protein-related peptide 3189.  
XX 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.  
XX Homo sapiens.  
XX W02003040340-A2.  
XX 15-MAY-2003.  
XX 07-NOV-2002; 2002WO-US036002.  
XX 07-NOV-2001; 2001US-00005480.  
XX 31-JAN-2002; 2002US-00062109.  
XX (AGEN-) AGENSYS INC.  
XX Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;  
XX Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;

PI Morrison RK, Challita-Eid PM;  
XX WPI; 2003-441560/41.  
XX A composition for diagnosing, preventing and treating cancer (e.g.  
XX prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides  
XX and polypeptides.  
XX Claim 13; Page 159; 135pp; English.  
XX This invention relates to a novel composition which comprises a substance  
XX that modulates the status of a novel human protein (161P2F10B) and its  
XX variants having a sequence of 875 amino acids provided in the  
XX specification. The protein of the invention is over-expressed in certain  
XX cancers. The compounds of the invention may have cytostatic activity and  
XX the sequence of the 161P2F10B protein, and the gene which encodes it, may  
XX be useful for gene therapy or the development of a vaccine. The  
XX composition and methods of the invention are useful in diagnosing,  
XX preventing and treating cancer. The present sequence is the amino acid  
XX sequence of a peptide which is derived from the sequence of the human  
XX 161P2F10B protein and which may be used in the development of the  
XX compounds of the invention.  
XX Sequence 10 AA;  
XX  
XX Query Match 58.0%; Score 29; DB 7; Length 10;  
XX Best Local Similarity 62.5%; Pred. No. 73;  
XX Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
XX  
XX 1 RFPDENFK 8  
XX |||:|  
XX 1 RKPQDHFK 8  
XX  
XX RESULT 18  
XX ADE66681  
XX ID ADE66681 standard; peptide; 10 AA.  
XX ADE66681;  
XX 29-JAN-2004 (first entry)  
XX Human 161P2F10B protein-related peptide 688.  
XX 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.  
XX Homo sapiens.  
XX W02003040340-A2.  
XX 15-MAY-2003.  
XX 07-NOV-2002; 2002WO-US036002.  
XX 07-NOV-2001; 2001US-00005480.  
XX 31-JAN-2002; 2002US-00062109.  
XX (AGEN-) AGENSYS INC.  
XX Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;  
XX Morrison RK, Challita-Eid PM;  
XX WPI; 2003-441560/41.  
XX A composition for diagnosing, preventing and treating cancer (e.g.  
XX prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides  
XX and polypeptides.  
XX Claim 13; Page 150; 135pp; English.  
XX This invention relates to a novel composition which comprises a substance  
XX that modulates the status of a novel human protein (161P2F10B) and its  
XX variants having a sequence of 875 amino acids provided in the



CC (osteoporosis). The compositions promote cell death and are useful for  
CC treating and/or ameliorating cancer and autoimmune diseases. The  
CC compounds are further useful for treating physiological impacts on organs  
CC caused by infection which induce cell death. (f) is useful to raise an  
CC immune response, as a reagent in assays designed to quantitatively  
CC determine levels of the protein in biological fluids, as markers for  
CC tissues in which the corresponding protein is expressed and to isolate  
CC receptors or ligands. AAU69571-AAU69736 represent the protective  
CC polypeptide sequences as described in the invention  
XX

SO Sequence 13 AA;

Query Match 58.0%; Score 29; DB 5; Length 13;  
Best Local Similarity 71.4%; Pred. No. 98;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FPDENFK 8  
|||:|  
Db 3 FPDENVK 9

## RESULT 21

ABP46673  
ID ABP46673 standard; peptide; 14 AA.

AC ABP46673;

DT 19-AUG-2002 (first entry)

DE Human Blys binding scFv VH CDR3 SEQ ID 2684.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
XX tumour necrosis factor; B cell proliferation; B cell differentiation;  
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
XX common variable immunodeficiency; acquired immunodeficiency syndrome.

OS Homo sapiens.

XX WO200202641-A1.

PD 10-JAN-2002.

PF 15-JUN-2001; 2001WO-US019110.

PR 16-JUN-2000; 2000US-0212210P.

PR 17-OCT-2000; 2000US-0240816P.

PR 16-MAR-2001; 2001US-0276248P.

PR 21-MAR-2001; 2001US-0277379P.

PR 25-MAY-2001; 2001US-0293499P.

XX (HUMA-) HUMAN GENOME SCI INC.

PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

PI WPI; 2002-114799/15.

DR WPI; 2002-114799/15.

XX Claim 2; Page 3032; 3148pp; English.

CC This invention describes novel antibodies that immunospecifically bind to  
CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the  
CC tumour necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have  
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
CC and so may be used to detect and quantitate the presence of Blys in  
CC biological samples and may be used in this way to diagnose disease

CC associated with aberrant expression of Blys. They may also be  
CC administered to treat diseases associated with aberrant Blys expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method of  
CC the invention  
XX

SO Sequence 14 AA;

Query Match 58.0%; Score 29; DB 5; Length 14;  
Best Local Similarity 62.5%; Pred. No. 1.1e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDENFKL 9  
|||:|  
Db 7 FPDHSFDL 14

## RESULT 22

ABP46426  
ID ABP46426 standard; peptide; 14 AA.

AC ABP46426;

DT 19-AUG-2002 (first entry)

DE Human Blys binding scFv VH CDR3 SEQ ID 2437.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
XX tumour necrosis factor; B cell proliferation; B cell differentiation;  
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
XX common variable immunodeficiency; acquired immunodeficiency syndrome.

OS Homo sapiens.

XX WO200202641-A1.

PD 10-JAN-2002.

PF 15-JUN-2001; 2001WO-US019110.

PR 16-JUN-2000; 2000US-0212210P.

PR 17-OCT-2000; 2000US-0240816P.

PR 16-MAR-2001; 2001US-0276248P.

PR 21-MAR-2001; 2001US-0277379P.

PR 25-MAY-2001; 2001US-0293499P.

XX (HUMA-) HUMAN GENOME SCI INC.

PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

PI WPI; 2002-114799/15.

DR WPI; 2002-114799/15.

XX Claim 2; Page 2990; 3148pp; English.

CC This invention describes novel antibodies that immunospecifically bind to  
CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the  
CC tumour necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have  
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
CC and so may be used to detect and quantitate the presence of Blys in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Blys. They may also be

CC administered to treat diseases associated with aberrant Blys expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent  
 CC the antibodies and fragments of the antibodies described in the method of  
 CC the invention

XX  
 XX  
 SQ Sequence 14 AA;

Query Match 58.0%; Score 29; DB 5; Length 14;  
 Best Local Similarity 62.5%; Pred. No. 1.1e+02;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDENFKL 9  
 |||:  
 DB 7 FPDSEFSL 14

RESULT 23  
 ABJ42183  
 ID ABJ42183 standard; peptide; 9 AA.  
 XX  
 AC ABJ42183;

DT 17-OCT-2003 (first entry)

DE 151P3D4 cancer gene related HLA peptide #3.

KM Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;  
 KM cellular immune response; adenocarcinoma; bladder; colorectal; lung;  
 KM bronchial; breast; carcinoma; human leukocyte antigen; HLA.

XX Homo sapiens.

OS WO200283860-A2.

PN 24-OCT-2002.

PD 09-APR-2002; 2002WO-US011644.

PF 10-APR-2001; 2001US-0282739P.

PR 25-APR-2001; 2001US-0286630P.

XX (AGEN-) AGENSYS INC.

PA Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison K;  
 PI Morrison RK, Ge W, Jakobovits A;

XX WPI; 2003-167091/16.

PT New 151P3D4 proteins and genes, useful for eliciting a humoral or  
 PT cellular immune response, or for diagnosing, prognosing, preventing or  
 PT treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer  
 PT or carcinoma.

XX Claim 13; Page 159; 426pp; English.

PS The invention relates to a novel composition comprising a substance that  
 CC modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or  
 CC a molecule that is modulated by the 151P3D4 protein, where the status of  
 CC a cell that expresses the 151P3D4 protein is modulated. The novel  
 CC compositions, or the 151P3D4 proteins and genes, are useful for eliciting  
 CC a humoral or cellular immune response. The 151P3D4 genes and proteins  
 CC are also useful for diagnosing, prognosing, preventing or treating  
 CC cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or  
 CC bronchial cancer, breast cancer or carcinoma. This sequence represents a  
 CC human leukocyte antigen peptide relating to the 151P3D4 composition of  
 CC the invention

XX Sequence 9 AA;

Query Match 56.0%; Score 28; DB 6; Length 9;

Best Local Similarity 62.5%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDENFKL 9  
 |||:  
 DB 1 FPDKXKHL 8

RESULT 24  
 ABJ41418  
 ID ABJ41418 standard; peptide; 9 AA.

XX  
 AC ABJ41418;

DT 17-OCT-2003 (first entry)

DE 151P3D4 cancer gene related peptide #2045.

KM Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;  
 KM cellular immune response; adenocarcinoma; bladder; colorectal; lung;  
 KM bronchial; breast; carcinoma.

XX Unidentified.

OS WO200283860-A2.

PN 24-OCT-2002.

PD 09-APR-2002; 2002WO-US011644.

PF 10-APR-2001; 2001US-0282739P.

PR 25-APR-2001; 2001US-0286630P.

XX (AGEN-) AGENSYS INC.

PA Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison K;  
 PI Morrison RK, Ge W, Jakobovits A;

XX WPI; 2003-167091/16.

PT New 151P3D4 proteins and genes, useful for eliciting a humoral or  
 PT cellular immune response, or for diagnosing, prognosing, preventing or  
 PT treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer  
 PT or carcinoma.

XX Claim 13; Page 147; 426pp; English.

PS The invention relates to a novel composition comprising a substance that  
 CC modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or  
 CC a molecule that is modulated by the 151P3D4 protein, where the status of  
 CC a cell that expresses the 151P3D4 protein is modulated. The novel  
 CC compositions, or the 151P3D4 proteins and genes, are useful for eliciting  
 CC a humoral or cellular immune response. The 151P3D4 genes and proteins  
 CC are also useful for diagnosing, prognosing, preventing or treating  
 CC cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or  
 CC bronchial cancer, breast cancer or carcinoma. This sequence represents a  
 CC 151P3D4 related peptide of the invention

XX Sequence 9 AA;

Query Match 56.0%; Score 28; DB 6; Length 9;  
 Best Local Similarity 62.5%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDENFKL 9  
 |||:  
 DB 2 FPDKXKHL 9

RESULT 25

ABJ44334  
 ID ABJ44334 standard; peptide; 9 AA.

XX

AC ABJ44334;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE 151P3D4 cancer gene related HLA peptide #2154.  
XX  
KW Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;  
XX cellular immune response; adenocarcinoma; bladder; colorectal; lung;  
XX bronchial; breast; carcinoma; human leukocyte antigen; HLA.  
XX  
OS Homo sapiens.  
XX  
PN WO200283860-A2.  
XX  
PD 24-OCT-2002.  
XX  
PF 09-APR-2002; 2002WO-US011644.  
XX  
PR 10-APR-2001; 2001US-0282739P.  
XX 25-APR-2001; 2001US-0286630P.  
XX  
PA (AGEN-) AGENSYS INC.  
XX  
PI Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison K;  
XX Morrison RK, Ge W, Jakobovits A;  
XX WPI; 2003-167091/16.  
XX  
DR New 151P3D4 proteins and genes, useful for eliciting a humoral or  
XX cellular immune response, or for diagnosing, prognosing, preventing or  
XX treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer  
XX or carcinoma.  
XX  
PS Claim 13; Page 179; 426pp; English.  
XX  
CC The invention relates to a novel composition comprising a substance that  
XX modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or  
XX a molecule that is modulated by the 151P3D4 protein, where the status of  
XX a cell that expresses the 151P3D4 protein is modulated. The novel  
XX compositions, or the 151P3D4 proteins and genes, are useful for eliciting  
XX a humoral or cellular immune response. The 151P3D4 genes and proteins  
XX are also useful for diagnosing, prognosing, preventing or treating  
XX cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or  
XX bronchial cancer, breast cancer or carcinoma. This sequence represents a  
XX human leukocyte antigen peptide relating to the 151P3D4 composition of  
XX the invention  
XX  
SQ Sequence 9 AA;  
XX  
Query Match 56.0%; Score 28; DB 6; Length 9;  
Best Local Similarity 62.5%; Pred. No. 1.4e+06;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 2 PPDENFKL 9  
DB 1 PPDKKHKL 8  
XX  
RESULT 26  
ABJ45672  
ID ABJ45672 standard; peptide; 9 AA.  
XX  
AC ABJ45672;  
XX  
DT 16-OCT-2003 (first entry)  
XX  
DE 151P3D4 cancer gene related HLA peptide #3492.  
XX  
KW Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;  
XX cellular immune response; adenocarcinoma; bladder; colorectal; lung;  
XX bronchial; breast; carcinoma; human leukocyte antigen; HLA.  
XX  
OS Homo sapiens.  
XX

XX  
PN WO200283860-A2.  
XX  
PD 24-OCT-2002.  
XX  
PF 09-APR-2002; 2002WO-US011644.  
XX  
PR 10-APR-2001; 2001US-0282739P.  
XX 25-APR-2001; 2001US-0286630P.  
XX  
PA (AGEN-) AGENSYS INC.  
XX  
PI Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison K;  
XX Morrison RK, Ge W, Jakobovits A;  
XX WPI; 2003-167091/16.  
XX  
DR New 151P3D4 proteins and genes, useful for eliciting a humoral or  
XX cellular immune response, or for diagnosing, prognosing, preventing or  
XX treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer  
XX or carcinoma.  
XX  
PS Claim 13; Page 192; 426pp; English.  
XX  
CC The invention relates to a novel composition comprising a substance that  
XX modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or  
XX a molecule that is modulated by the 151P3D4 protein, where the status of  
XX a cell that expresses the 151P3D4 protein is modulated. The novel  
XX compositions, or the 151P3D4 proteins and genes, are useful for eliciting  
XX a humoral or cellular immune response. The 151P3D4 genes and proteins  
XX are also useful for diagnosing, prognosing, preventing or treating  
XX cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or  
XX bronchial cancer, breast cancer or carcinoma. This sequence represents a  
XX human leukocyte antigen peptide relating to the 151P3D4 composition of  
XX the invention  
XX  
SQ Sequence 9 AA;  
XX  
Query Match 56.0%; Score 28; DB 6; Length 9;  
Best Local Similarity 62.5%; Pred. No. 1.4e+06;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 2 PPDENFKL 9  
DB 2 PPDKKHKL 9  
XX  
RESULT 27  
ABJ47747  
ID ABJ47747 standard; peptide; 9 AA.  
XX  
AC ABJ47747;  
XX  
DT 16-OCT-2003 (first entry)  
XX  
DE 151P3D4 cancer gene related HLA peptide #5567.  
XX  
KW Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;  
XX cellular immune response; adenocarcinoma; bladder; colorectal; lung;  
XX bronchial; breast; carcinoma; human leukocyte antigen; HLA.  
XX  
OS Homo sapiens.  
XX  
PN WO200283860-A2.  
XX  
PD 24-OCT-2002.  
XX  
PF 09-APR-2002; 2002WO-US011644.  
XX  
PR 10-APR-2001; 2001US-0282739P.  
XX 25-APR-2001; 2001US-0286630P.  
XX  
PA (AGEN-) AGENSYS INC.  
XX



XX Chailita-Bid PM, Raitano AB, Faris M, Hubert RS, Morrison K;  
PI Morrison RK, Ge W, Jakobovits A;  
XX WPI; 2003-167091/16.  
XX New 151P3D4 proteins and genes, useful for eliciting a humoral or  
PT cellular immune response, or for diagnosing, prognosing, preventing or  
PT treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer  
PT or carcinoma.  
XX Claim 13; Page 212; 426pp; English.  
XX The invention relates to a novel composition comprising a substance that  
CC modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or  
CC a molecule that is modulated by the 151P3D4 protein, where the status of  
CC a cell that expresses the 151P3D4 protein is modulated. The novel  
CC compositions, or the 151P3D4 proteins and genes, are useful for eliciting  
CC a humoral or cellular immune response. The 151P3D4 genes and proteins  
CC are also useful for diagnosing, prognosing, preventing or treating  
CC cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or  
CC bronchial cancer, breast cancer or carcinoma. This sequence represents a  
CC human leukocyte antigen peptide relating to the 151P3D4 composition of  
CC the invention  
XX  
SQ Sequence 9 AA;  
Query Match 56.0%; Score 28; DB 6; Length 9;  
Best Local Similarity 62.5%; Pred. No. 1.4e+06;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 2 FPDENFKL 9  
|||:  
2 FPDKKHKL 9  
Db  
RESULT 28  
ABU49116  
ID ABU49116 standard; peptide; 9 AA.  
XX  
AC ABU49116;  
XX  
DT 16-OCT-2003 (first entry)  
XX  
DE 151P3D4 cancer gene related HLA peptide #6936.  
XX  
KW Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;  
KW cellular immune response; adenocarcinoma; bladder; colorectal; lung;  
KW bronchial; breast; carcinoma; human leukocyte antigen; HLA.  
XX  
OS Homo sapiens.  
XX  
PN WO200283860-A2.  
XX  
PD 24-OCT-2002.  
XX  
PF 09-APR-2002; 2002WO-US011644.  
XX  
PR 10-APR-2001; 2001US-0282739P.  
PR 25-APR-2001; 2001US-0286630P.  
XX  
PA (AGEN-) AGENSYS INC.  
XX  
PI Chailita-Bid PM, Raitano AB, Faris M, Hubert RS, Morrison K;  
PI Morrison RK, Ge W, Jakobovits A;  
XX WPI; 2003-167091/16.  
XX New 151P3D4 proteins and genes, useful for eliciting a humoral or  
PT cellular immune response, or for diagnosing, prognosing, preventing or  
PT treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer  
PT or carcinoma.  
XX

PS Claim 13; Page 225; 426pp; English.  
XX The invention relates to a novel composition comprising a substance that  
CC modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or  
CC a molecule that is modulated by the 151P3D4 protein, where the status of  
CC a cell that expresses the 151P3D4 protein is modulated. The novel  
CC compositions, or the 151P3D4 proteins and genes, are useful for eliciting  
CC a humoral or cellular immune response. The 151P3D4 genes and proteins  
CC are also useful for diagnosing, prognosing, preventing or treating  
CC cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or  
CC bronchial cancer, breast cancer or carcinoma. This sequence represents a  
CC human leukocyte antigen peptide relating to the 151P3D4 composition of  
CC the invention  
XX  
SQ Sequence 9 AA;  
Query Match 56.0%; Score 28; DB 6; Length 9;  
Best Local Similarity 62.5%; Pred. No. 1.4e+06;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 2 FPDENFKL 9  
|||:  
1 FPDKKHKL 8  
Db  
RESULT 29  
ABU41779  
ID ABU41779 standard; peptide; 9 AA.  
XX  
AC ABU41779;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE 151P3D4 cancer gene related peptide #2406.  
XX  
KW Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;  
KW cellular immune response; adenocarcinoma; bladder; colorectal; lung;  
KW bronchial; breast; carcinoma.  
XX  
OS Unidentified.  
XX  
PN WO200283860-A2.  
XX  
PD 24-OCT-2002.  
XX  
PF 09-APR-2002; 2002WO-US011644.  
XX  
PR 10-APR-2001; 2001US-0282739P.  
PR 25-APR-2001; 2001US-0286630P.  
XX  
PA (AGEN-) AGENSYS INC.  
XX  
PI Chailita-Bid PM, Raitano AB, Faris M, Hubert RS, Morrison K;  
PI Morrison RK, Ge W, Jakobovits A;  
XX WPI; 2003-167091/16.  
XX New 151P3D4 proteins and genes, useful for eliciting a humoral or  
PT cellular immune response, or for diagnosing, prognosing, preventing or  
PT treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer  
PT or carcinoma.  
XX  
PS Claim 13; Page 151; 426pp; English.  
XX The invention relates to a novel composition comprising a substance that  
CC modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or  
CC a molecule that is modulated by the 151P3D4 protein, where the status of  
CC a cell that expresses the 151P3D4 protein is modulated. The novel  
CC compositions, or the 151P3D4 proteins and genes, are useful for eliciting  
CC a humoral or cellular immune response. The 151P3D4 genes and proteins  
CC are also useful for diagnosing, prognosing, preventing or treating  
CC cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or  
CC bronchial cancer, breast cancer or carcinoma. This sequence represents a

CC 151P3D4 related peptide of the invention  
XX  
SQ Sequence 9 AA;  
Query Match 56.0%; Score 28; DB 6; Length 9;  
Best Local Similarity 62.5%; Pred. No. 1.4e+06;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 2 PPDENFKL 9  
|||: |||  
1 PPDKKHKL 8  
Db  
RESULT 30  
ABJ41872  
ID ABJ41872 standard; peptide: 9 AA.  
XX  
AC ABJ41872;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE 151P3D4 cancer gene related peptide #2459.  
XX  
KW Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;  
KW cellular immune response; adenocarcinoma; bladder; colorectal; lung;  
KW bronchial; breast; carcinoma.  
XX  
OS Unidentified.  
XX  
PN WO200283860-A2.  
XX  
PD 24-OCT-2002.  
XX  
PF 09-APR-2002; 2002WO-US011644.  
XX  
PR 10-APR-2001; 2001US-0282739P.  
XX  
PR 25-APR-2001; 2001US-0286630P.  
XX  
PA (AGEN-) AGENSYS INC.  
XX  
PI Chailita-Bid PM, Raitano AB, Farris M, Hubert RS, Morrison K;  
PI Morrison RK, Ge W, Jakobovits A;  
XX  
DR WPI; 2003-167091/16.  
XX  
PT New 151P3D4 proteins and genes, useful for eliciting a humoral or  
PT cellular immune response, or for diagnosing, prognosing, preventing or  
PT treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer  
PT or carcinoma.  
XX  
PS Claim 13; Page 151; 426pp; English.  
XX  
XX The invention relates to a novel composition comprising a substance that  
CC modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or  
CC a molecule that is modulated by the 151P3D4 protein, where the status of  
CC a cell that expresses the 151P3D4 protein is modulated. The novel  
CC compositions, or the 151P3D4 proteins and genes, are useful for eliciting  
CC a humoral or cellular immune response. The 151P3D4 genes and proteins  
CC are also useful for diagnosing, prognosing, preventing or treating  
CC cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or  
CC bronchial cancer, breast cancer or carcinoma. This sequence represents a  
CC 151P3D4 related peptide of the invention  
XX  
SQ Sequence 9 AA;  
Query Match 56.0%; Score 28; DB 6; Length 9;  
Best Local Similarity 62.5%; Pred. No. 1.4e+06;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 2 PPDENFKL 9  
|||: |||  
2 PPDKKHKL 9  
Db

RESULT 31  
ABJ47004  
ID ABJ47004 standard; peptide: 9 AA.  
XX  
AC ABJ47004;  
XX  
DT 16-OCT-2003 (first entry)  
XX  
DE 151P3D4 cancer gene related HLA peptide #4824.  
XX  
KW Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;  
KW cellular immune response; adenocarcinoma; bladder; colorectal; lung;  
KW bronchial; breast; carcinoma; human leukocyte antigen; HLA.  
XX  
OS Homo sapiens.  
XX  
PN WO200283860-A2.  
XX  
PD 24-OCT-2002.  
XX  
PF 09-APR-2002; 2002WO-US011644.  
XX  
PR 10-APR-2001; 2001US-0282739P.  
XX  
PR 25-APR-2001; 2001US-0286630P.  
XX  
PA (AGEN-) AGENSYS INC.  
XX  
PI Chailita-Bid PM, Raitano AB, Farris M, Hubert RS, Morrison K;  
PI Morrison RK, Ge W, Jakobovits A;  
XX  
DR WPI; 2003-167091/16.  
XX  
PT New 151P3D4 proteins and genes, useful for eliciting a humoral or  
PT cellular immune response, or for diagnosing, prognosing, preventing or  
PT treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer  
PT or carcinoma.  
XX  
PS Claim 13; Page 205; 426pp; English.  
XX  
XX The invention relates to a novel composition comprising a substance that  
CC modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or  
CC a molecule that is modulated by the 151P3D4 protein, where the status of  
CC a cell that expresses the 151P3D4 protein is modulated. The novel  
CC compositions, or the 151P3D4 proteins and genes, are useful for eliciting  
CC a humoral or cellular immune response. The 151P3D4 genes and proteins  
CC are also useful for diagnosing, prognosing, preventing or treating  
CC cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or  
CC bronchial cancer, breast cancer or carcinoma. This sequence represents a  
CC human leukocyte antigen peptide relating to the 151P3D4 composition of  
CC the invention  
XX  
SQ Sequence 9 AA;  
Query Match 56.0%; Score 28; DB 6; Length 9;  
Best Local Similarity 62.5%; Pred. No. 1.4e+06;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 2 PPDENFKL 9  
|||: |||  
2 PPDKKHKL 9  
Db  
RESULT 32  
ABJ39404  
ID ABJ39404 standard; peptide: 9 AA.  
XX  
AC ABJ39404;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE 151P3D4 cancer gene related peptide #31.  
XX

KM Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;  
 KW cellular immune response; adenocarcinoma; bladder; colorectal; lung;  
 XX bronchial; breast; carcinoma.  
 XX Unidentified.  
 OS  
 XX WO200283860-A2.  
 PN  
 XX 24-OCT-2002.  
 PD  
 XX 09-APR-2002; 2002WO-US011644.  
 PF  
 XX 10-APR-2001; 2001US-0282739P.  
 PR  
 XX 25-APR-2001; 2001US-0286630P.  
 XX  
 XX (AGEN-) AGENSYS INC.  
 PA  
 XX Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison K;  
 PI Morrison RK, Ge W, Jakobovits A;  
 XX WPI; 2003-167091/16.  
 DR  
 XX New 151P3D4 proteins and genes, useful for eliciting a humoral or  
 PT cellular immune response, or for diagnosing, prognosing, preventing or  
 PT treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer  
 PT or carcinoma.  
 PS  
 XX Claim 13; Page 127; 426pp; English.  
 CC The invention relates to a novel composition comprising a substance that  
 CC modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or  
 CC a molecule that is modulated by the 151P3D4 protein, where the status of  
 CC a cell that expresses the 151P3D4 protein is modulated. The novel  
 CC compositions, or the 151P3D4 proteins and genes, are useful for eliciting  
 CC a humoral or cellular immune response. The 151P3D4 genes and proteins  
 CC are also useful for diagnosing, prognosing, preventing or treating  
 CC cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or  
 CC bronchial cancer, breast cancer or carcinoma. This sequence represents a  
 CC 151P3D4 related peptide of the invention  
 CC  
 SQ Sequence 9 AA;  
 QY  
 DB 2 FPDENFKL 9  
 1 FPKKHKL 8  
 RESULT 33  
 ABJ44281  
 ID ABJ44281 standard; peptide; 9 AA.  
 XX  
 AC ABJ44281;  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX  
 DE 151P3D4 cancer gene related HLA peptide #2101.  
 XX  
 KW Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;  
 KW cellular immune response; adenocarcinoma; bladder; colorectal; lung;  
 KW bronchial; breast; carcinoma; human leukocyte antigen, HLA.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200283860-A2.  
 PN  
 XX 24-OCT-2002.  
 PD  
 XX 09-APR-2002; 2002WO-US011644.  
 PF  
 XX 10-APR-2001; 2001US-0282739P.  
 PR  
 XX 25-APR-2001; 2001US-0286630P.  
 XX  
 XX (AGEN-) AGENSYS INC.  
 PA  
 XX Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison K;  
 PI Morrison RK, Ge W, Jakobovits A;  
 XX WPI; 2003-167091/16.  
 DR  
 XX New 151P3D4 proteins and genes, useful for eliciting a humoral or  
 PT cellular immune response, or for diagnosing, prognosing, preventing or  
 PT treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer  
 PT or carcinoma.  
 PS  
 XX Claim 13; Page 127; 426pp; English.  
 CC The invention relates to a novel composition comprising a substance that  
 CC modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or  
 CC a molecule that is modulated by the 151P3D4 protein, where the status of  
 CC a cell that expresses the 151P3D4 protein is modulated. The novel  
 CC compositions, or the 151P3D4 proteins and genes, are useful for eliciting  
 CC a humoral or cellular immune response. The 151P3D4 genes and proteins  
 CC are also useful for diagnosing, prognosing, preventing or treating  
 CC cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or  
 CC bronchial cancer, breast cancer or carcinoma. This sequence represents a  
 CC human leukocyte antigen peptide relating to the 151P3D4 composition of  
 CC the invention  
 CC  
 SQ Sequence 9 AA;  
 QY  
 DB 2 FPDENFKL 9  
 1 FPKKHKL 8  
 RESULT 34  
 ABJ45005  
 ID ABJ45005 standard; peptide; 9 AA.  
 XX  
 AC ABJ45005;  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX  
 DE 151P3D4 cancer gene related HLA peptide #2825.  
 XX  
 KW Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;  
 KW cellular immune response; adenocarcinoma; bladder; colorectal; lung;  
 KW bronchial; breast; carcinoma; human leukocyte antigen, HLA.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200283860-A2.  
 PN  
 XX 24-OCT-2002.  
 PD  
 XX 09-APR-2002; 2002WO-US011644.  
 PF  
 XX 10-APR-2001; 2001US-0282739P.  
 PR  
 XX 25-APR-2001; 2001US-0286630P.  
 XX  
 XX (AGEN-) AGENSYS INC.  
 PA  
 XX Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison K;  
 PI Morrison RK, Ge W, Jakobovits A;  
 XX WPI; 2003-167091/16.  
 DR  
 XX New 151P3D4 proteins and genes, useful for eliciting a humoral or

PR 10-APR-2001; 2001US-0282739P.  
 PR 25-APR-2001; 2001US-0286630P.  
 XX  
 XX (AGEN-) AGENSYS INC.  
 PA  
 XX Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison K;  
 PI Morrison RK, Ge W, Jakobovits A;  
 XX WPI; 2003-167091/16.  
 DR  
 XX New 151P3D4 proteins and genes, useful for eliciting a humoral or  
 PT cellular immune response, or for diagnosing, prognosing, preventing or  
 PT treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer  
 PT or carcinoma.  
 PS  
 XX Claim 13; Page 179; 426pp; English.  
 CC The invention relates to a novel composition comprising a substance that  
 CC modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or  
 CC a molecule that is modulated by the 151P3D4 protein, where the status of  
 CC a cell that expresses the 151P3D4 protein is modulated. The novel  
 CC compositions, or the 151P3D4 proteins and genes, are useful for eliciting  
 CC a humoral or cellular immune response. The 151P3D4 genes and proteins  
 CC are also useful for diagnosing, prognosing, preventing or treating  
 CC cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or  
 CC bronchial cancer, breast cancer or carcinoma. This sequence represents a  
 CC human leukocyte antigen peptide relating to the 151P3D4 composition of  
 CC the invention  
 CC  
 SQ Sequence 9 AA;  
 QY  
 DB 2 FPDENFKL 9  
 2 FPKKHKL 9  
 RESULT 34  
 ABJ45005  
 ID ABJ45005 standard; peptide; 9 AA.  
 XX  
 AC ABJ45005;  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX  
 DE 151P3D4 cancer gene related HLA peptide #2825.  
 XX  
 KW Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;  
 KW cellular immune response; adenocarcinoma; bladder; colorectal; lung;  
 KW bronchial; breast; carcinoma; human leukocyte antigen, HLA.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200283860-A2.  
 PN  
 XX 24-OCT-2002.  
 PD  
 XX 09-APR-2002; 2002WO-US011644.  
 PF  
 XX 10-APR-2001; 2001US-0282739P.  
 PR  
 XX 25-APR-2001; 2001US-0286630P.  
 XX  
 XX (AGEN-) AGENSYS INC.  
 PA  
 XX Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison K;  
 PI Morrison RK, Ge W, Jakobovits A;  
 XX WPI; 2003-167091/16.  
 DR  
 XX New 151P3D4 proteins and genes, useful for eliciting a humoral or

PT cellular immune response, or for diagnosing, prognosing, preventing or  
PT treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer  
PT or carcinoma.  
XX  
PS Claim 13; Page 186; 426pp; English.  
XX  
CC The invention relates to a novel composition comprising a substance that  
CC modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or  
CC a molecule that is modulated by the 151P3D4 protein, where the status of  
CC a cell that expresses the 151P3D4 protein is modulated. The novel  
CC compositions, or the 151P3D4 proteins and genes, are useful for eliciting  
CC a humoral or cellular immune response. The 151P3D4 genes and proteins  
CC are also useful for diagnosing, prognosing, preventing or treating  
CC cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or  
CC bronchial cancer, breast cancer or carcinoma. This sequence represents a  
CC human leukocyte antigen peptide relating to the 151P3D4 composition of  
CC the invention  
XX  
SQ Sequence 9 AA;  
XX  
Query Match 56.0%; Score 28; DB 6; Length 9;  
Best Local Similarity 62.5%; Pred. No. 1.4e+06;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
OY 2 PPDENFKL 9  
DB 1 PPDKKHKL 8  
XX  
RESULT 35  
ABU45032  
ID ABU45032 standard; peptide; 9 AA.  
XX  
AC ABU45032;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE 151P3D4 cancer gene related HLA peptide #2852.  
XX  
KM Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;  
KM cellular immune response; adenocarcinoma; bladder; colorectal; lung;  
KW bronchial; breast; carcinoma; human leukocyte antigen; HLA.  
XX  
OS Homo sapiens.  
XX  
PN WO200283860-A2.  
XX  
PD 24-OCT-2002.  
XX  
PF 09-APR-2002; 2002WO-US011644.  
XX  
PR 10-APR-2001; 2001US-0282739P.  
PR 25-APR-2001; 2001US-0286630P.  
XX  
PA (AGEN-) AGENSYS INC.  
XX  
PI Chailita-Bid PM, Raitano AB, Farie W, Hubert RS, Morrison K;  
PI Morrison RK, Ge W, Jakobovits A;  
XX  
DR WPI; 2003-167091/16.  
XX  
XX New 151P3D4 proteins and genes, useful for eliciting a humoral or  
PT cellular immune response, or for diagnosing, prognosing, preventing or  
PT treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer  
PT or carcinoma.  
XX  
PS Claim 13; Page 186; 426pp; English.  
XX  
CC The invention relates to a novel composition comprising a substance that  
CC modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or  
CC a molecule that is modulated by the 151P3D4 protein, where the status of  
CC a cell that expresses the 151P3D4 protein is modulated. The novel  
CC compositions, or the 151P3D4 proteins and genes, are useful for eliciting

CC a humoral or cellular immune response. The 151P3D4 genes and proteins  
CC are also useful for diagnosing, prognosing, preventing or treating  
CC cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or  
CC bronchial cancer, breast cancer or carcinoma. This sequence represents a  
CC human leukocyte antigen peptide relating to the 151P3D4 composition of  
CC the invention  
XX  
SQ Sequence 9 AA;  
XX  
Query Match 56.0%; Score 28; DB 6; Length 9;  
Best Local Similarity 62.5%; Pred. No. 1.4e+06;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
OY 2 PPDENFKL 9  
DB 2 PPDKKHKL 9  
XX  
RESULT 36  
ABU48393  
ID ABU48393 standard; peptide; 9 AA.  
XX  
AC ABU48393;  
XX  
DT 16-OCT-2003 (first entry)  
XX  
DE 151P3D4 cancer gene related HLA peptide #6213.  
XX  
KM Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;  
KM cellular immune response; adenocarcinoma; bladder; colorectal; lung;  
KW bronchial; breast; carcinoma; human leukocyte antigen; HLA.  
XX  
OS Homo sapiens.  
XX  
PN WO200283860-A2.  
XX  
PD 24-OCT-2002.  
XX  
PF 09-APR-2002; 2002WO-US011644.  
XX  
PR 10-APR-2001; 2001US-0282739P.  
PR 25-APR-2001; 2001US-0286630P.  
XX  
PA (AGEN-) AGENSYS INC.  
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PI Chailita-Bid PM, Raitano AB, Farie W, Hubert RS, Morrison K;  
PI Morrison RK, Ge W, Jakobovits A;  
XX  
DR WPI; 2003-167091/16.  
XX  
XX New 151P3D4 proteins and genes, useful for eliciting a humoral or  
PT cellular immune response, or for diagnosing, prognosing, preventing or  
PT treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer  
PT or carcinoma.  
XX  
PS Claim 13; Page 218; 426pp; English.  
XX  
CC The invention relates to a novel composition comprising a substance that  
CC modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or  
CC a molecule that is modulated by the 151P3D4 protein, where the status of  
CC a cell that expresses the 151P3D4 protein is modulated. The novel  
CC compositions, or the 151P3D4 proteins and genes, are useful for eliciting  
CC a humoral or cellular immune response. The 151P3D4 genes and proteins  
CC are also useful for diagnosing, prognosing, preventing or treating  
CC cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or  
CC bronchial cancer, breast cancer or carcinoma. This sequence represents a  
CC human leukocyte antigen peptide relating to the 151P3D4 composition of  
CC the invention  
XX  
SQ Sequence 9 AA;  
XX  
Query Match 56.0%; Score 28; DB 6; Length 9;  
Best Local Similarity 62.5%; Pred. No. 1.4e+06;